



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 180248

**TO: Sean McGarry**  
**Art Unit: 1635**  
**Location: REM/2D19/2C19**  
**Serial Number: 10/655801**

**Friday, March 03, 2006**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

#### Published Applications Database - November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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STIC-Biotech/ChemLib

180248

44  
ARF

From: McGarry, Sean  
Sent: Wednesday, February 22, 2006 3:13 PM  
To: STIC-Biotech/ChemLib  
Subject: SEQ SEARCH 10/655,801

Sean McGarry  
AU 1635  
REM 02D19 Office  
REM 2C18 Mailbox  
X20761  
73484

10/655,801

Please, a length limited search of SEQ ID NOS: 19-22 and nucleotides 14-177 of SEQ ID NO: 3 (nt  $\leq$  80).

Thank You.

mg  
19 na 18  
20 18  
21 18  
22 18  
3 na 4145

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
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Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

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Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_  
Searcher: Beverly e 2528  
Terminal time: \_\_\_\_\_  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: \_\_\_\_\_  
Number of Searches: \_\_\_\_\_  
Number of Databases: \_\_\_\_\_

Search Site  
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\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
Type of Search  
\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
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\_\_\_\_ SDC  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: March 3, 2006, 07:16:16 ; Search time 3434.27 Seconds  
(without alignments)  
2714.499 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sv.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	16.5	75	6	AX391505 Sequence
2	27	16.5	75	6	AX391607 Sequence
3	25.4	15.5	75	6	AX391506 Sequence
4	25.4	15.5	75	6	AX391608 Sequence
5	23.6	14.4	65	6	CQ556308 Sequence
6	22	13.4	65	6	CQ534115 Sequence
7	21.8	13.3	78	6	AR101987 Sequence
8	21.8	13.3	78	6	BD064232 Therapy f
9	21.8	13.3	78	6	CS105031 Sequence
10	21.8	13.3	78	6	AR322465 Sequence
11	21.8	13.3	78	6	AR372141 Sequence
12	21.8	13.3	78	8	HUNGHPA
13	21.8	13.3	80	6	I00999 Sequence 2
14	21.8	13.3	80	6	I02190 Sequence 2
15	21.4	13.0	65	6	CQ554646 Sequence
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17	21	12.8	75	11	CS001411 Sequence
18	20.6	12.6	50	6	CS063833 Sequence

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21	20.6	12.6	69	8	AF189414 Homo sapi
22	20.6	12.6	75	11	CS001427 Sequence
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55	19.4	11.8	60	6	CQ561796 Sequence
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## ALIGNMENTS

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 LOCUS AX391505 75 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 16 from Patent EP1184391.  
 ACCESSION AX391505  
 VERSION AX391505.1 GI:19700113  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.  
 TITLE Acetylcholine receptor subunits  
 JOURNAL Patent: EP 1184391-A 16 06-MAR-2002;  
 BAYER AG (DE)  
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 DB 1 GCGGGAGTGGGTGCATCTTAGAGTCCCGCGCTTCGCAAGAAAGTTTATACATGCT 60  
 QY 78 TTGACTGTCTCTTACC 92  
 DB 61 GCGACGAGCCCTACC 75

RESULT 2  
 AX391607  
 LOCUS AX391607 75 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 20 from Patent EP1184390.  
 ACCESSION AX391607  
 VERSION AX391607.1 GI:19700213  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.  
 TITLE Acetylcholine receptor subunits  
 JOURNAL Patent: EP 1184390-A 20 06-MAR-2002;  
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 LOCUS AX391506 75 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 17 from Patent EP1184391.  
 ACCESSION AX391506  
 VERSION AX391506.1 GI:19700114  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.  
 TITLE Acetylcholine receptor subunits  
 JOURNAL Patent: EP 1184391-A 17 06-MAR-2002;  
 BAYER AG (DE)  
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 DEFINITION Sequence 21 from Patent EP1184390.  
 ACCESSION AX391608  
 VERSION AX391608.1 GI:19700214  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.  
 TITLE Acetylcholine receptor subunits  
 JOURNAL Patent: EP 1184390-A 21 06-MAR-2002;  
 BAYER AG (DE)  
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P GILLESPIE, CAROL M
PI KINOSHITA,
PI DOUGLAS A TRECO, MELANIE D WILLIAMS
PC C12N9/40, C12N15/62, C12N15/56, A61K38/47, A61K48/00, C12N5/10 CC
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DEFINITION Sequence 22 from Patent EP1538202.
ACCESSION CS105031
VERSION CS105031.1 GI:67512962
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Selden, R.F., Borowski, M., Treco, D.A., Gillespie, F.P.,
Kinoshita, C.M. and Williams, M.D.
TITLE Production of human alpha-galactosidase A
JOURNAL Patent: EP 1538202-A 22 08-JUN-2005;
Transkaryotic Therapies, Inc. (US)
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RESULT 10
LOCUS AR322465 78 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6566099.
ACCESSION AR322465
VERSION AR322465.1 GI:33708230
KEYWORDS
SOURCE Unknown.

PR 13-SEP-1996 US 08/712614
PI RICHARD F SELDEN, MARIANNE BOROWSKI, FRANCES
P GILLESPIE, CAROL M
PI KINOSHITA,
PI DOUGLAS A TRECO, MELANIE D WILLIAMS
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LOCUS AR372141 78 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 22 from patent US 6395884.
ACCESSION AR372141
VERSION AR372141.1 GI:34609450
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 78)
AUTHORS Selden, R.F., Borowski, M., Gillespie, F.P., Kinoshita, C.M.,
Treco, D.A. and Williams, M.D.
TITLE Therapy for .alpha.-galactosidase a deficiency
JOURNAL Patent: US 6395884-A 22 28-MAY-2002;
Transkaryotic Therapies, Inc.; DE
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RESULT 12
LOCUS HUMGHPA 78 bp mRNA linear PRI 08-NOV-1994
DEFINITION Human precursor growth hormone mRNA, 5' end.
ACCESSION M14398
VERSION M14398.1 GI:183158
KEYWORDS growth hormone.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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ACCESSION	102190			
VERSION	102190.1	GI:270293		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 80)			
AUTHORS	Gray,G.L. and Heyneker,H.L.			
TITLE	Recombinant procaryotic cell containing correctly processed human growth hormone			
JOURNAL	Patent: US 4859600-A 2 22-AUG-1989;			
FEATURES	Genentech, Inc.; South San Francisco, CA			
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ACCESSION Q0554646  
VERSION Q0554646.1 GI:41521073  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE 1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,I. and Patgler,S.  
AUTHORS Oligonucleotide library for detecting rna transcripts and splice  
TITLE variants that populate a transcriptome  
JOURNAL Patent: WO 0210449-A 24281 07-FEB-2002;  
CompuGen Inc. (US)  
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 DEFINITION Sequence 492 from Patent WO0210449.  
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 VERSION CQ530857.1 GI:41497121  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 REFERENCE 1  
 AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome  
 JOURNAL Patent: WO 0210449-A 492 07-FEB-2002;  
 Compugen Inc. (US)  
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 Best Local Similarity 69.0%; Pred. No. 1.2e+05;  
 Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 58 GGCACAGTCTCTCTGTTGACTGCTCTTACCCCGGGA 99  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 42 GTCACCTGCTCTCTCTGTTGACTGCTCTTACCCCTGTGA 1  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 RESULT 17  
 CS001411/c  
 LOCUS CS001411 75 bp DNA linear SYN 01-FEB-2005  
 DEFINITION Sequence 172 from Patent WO2005005462.  
 ACCESSION CS001411  
 VERSION CS001411.1 GI:58423889  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Chan,A.C., Gordon,N.C., Kelley,R.F., Koehler,M.F. and  
 Scarovasnik,M.A.  
 TITLE Blys antagonists and uses thereof  
 JOURNAL Patent: WO 2005005462-A 20-JAN-2005;  
 Genentech, Inc. (US)  
 FEATURES source  
 Location/Qualifiers  
 1..75  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Clone 52,71"  
 ORIGIN  
 Query Match 12.8%; Score 21; DB 11; Length 75;  
 Best Local Similarity 82.8%; Pred. No. 1.3e+05;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 TCGGCCACCTTGTGATGAGGGGACTGGCA 31  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 72 TCCTCACCTTGTGATGAGGTGACAGGGCA 44  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 RESULT 18  
 CS063833  
 LOCUS CS063833 50 bp DNA linear PAT 20-APR-2005  
 DEFINITION Sequence 22 from Patent WO2005030963.  
 ACCESSION CS063833  
 VERSION CS063833.1 GI:62817056  
 KEYWORDS

SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Dupraz,P. and Kobr,M.  
 TITLE Leader sequences for use in production of proteins  
 JOURNAL Patent: WO 2005030963-A 22 07-APR-2005;  
 Applied Research Systems ARS Holding N.V. (AN)  
 FEATURES source  
 Location/Qualifiers  
 1..50  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 ORIGIN  
 Query Match 12.6%; Score 20.6; DB 6; Length 50;  
 Best Local Similarity 67.4%; Pred. No. 1.8e+05;  
 Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 QY 72 CCTGGTTTCACTGCTCTTACCCCGGGAGGAGTCAGCCAGC 114  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 2 CCTGCTGTGCTCCCTGCTGCTGAGGAGGCGCAGCCAGC 44  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 RESULT 19  
 CQ534582  
 LOCUS CQ534582 65 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 4217 from Patent WO0210449.  
 ACCESSION CQ534582  
 VERSION CQ534582.1 GI:41500846  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 REFERENCE 1  
 AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome  
 JOURNAL Patent: WO 0210449-A 4217 07-FEB-2002;  
 Compugen Inc. (US)  
 FEATURES source  
 Location/Qualifiers  
 1..65  
 /organism="Rattus norvegicus"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:10116"  
 ORIGIN  
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 Best Local Similarity 62.7%; Pred. No. 1.8e+05;  
 Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 QY 40 CAGTCCCGAAGTTCTCAGGCACAGGTCTCTCTCTGTTGACTGCTCTTA 90  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 6 CAGTGAAGCAGATCTTCAGAGACAGACATCTCTCTGTTAGGACTCTTA 56  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 RESULT 20  
 CQ558604  
 LOCUS CQ558604 65 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 28239 from Patent WO0210449.  
 ACCESSION CQ558604  
 VERSION CQ558604.1 GI:41525031  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 REFERENCE 1  
 AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
 TITLE Oligonucleotide library for detecting rna transcripts and splice

variants that populate a transcriptome  
Patent: WO 0210449-A 28239 07-FEB-2002;  
CompuGen Inc. (US)

## FEATURES

source  
Location/Qualifiers  
1..65  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

## ORIGIN

Query Match 12.6%; Score 20.6; DB 6; Length 65;  
Best Local Similarity 67.4%; Pred. No. 1.8e+05;  
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 97 GGGAGCAGTCAGCAGCTGCAAGCCCAAGTGAAGACATC 139  
|||||  
DB 10 GGTGCACTGAAGCTGTTGAAAGCACCATGGAGAACTTC 52  
|||||

## RESULT 21

AF189414  
LOCUS  
DEFINITION Homo sapiens clone B301U T-cell receptor beta chain (TCRBV20S1)  
mRNA, partial cds.

ACCESSION AF189414  
VERSION AF189414.1 GI:6841695  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)

REFERENCE  
AUTHORS Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U., Ringuelette,N., Samson,J., Lapointe,N. and Sekaly,R.P.  
TITLE Transient T cell receptor beta-chain variable region-specific expansions of CD4+ and CD8+ T cells during the early phase of pediatric human immunodeficiency virus infection: characterization of expanded cell populations by T cell receptor phenotyping

J. Infect. Dis. 181 (1), 107-120 (2000)  
10608757  
2 (bases 1 to 69)  
Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U., Ringuelette,N., Samson,J., Lapointe,N. and Sekaly,R.P.  
Direct Submission  
Submitted (24-SEP-1999) Laboratoire d'immunologie, IRCM, 110 avenue Des Pins ouest, Montreal, Quebec H2W 1R7, Canada

## FEATURES

source  
Location/Qualifiers  
1..69  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="B301U"  
<1..>69  
/gene="TCRBV20S1"  
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/note="V(D)J region"  
/codon\_start=1  
/product="T-cell receptor beta chain"  
/protein\_id="AAF29201.1"  
/db\_xref="GI:6841696"  
/translation="LLSDSGFVLCAMSVYINTGELFF"

## gene

## CDS

## ORIGIN

Query Match 12.6%; Score 20.6; DB 8; Length 69;  
Best Local Similarity 74.3%; Pred. No. 1.8e+05;  
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 66 TCTCTTCCTGGTTGACTGCTTACCCGGGGAG 100  
|||||  
DB 26 TCTGTCCTGGAGTGTCTATCTTAACACCGGGGAG 60  
|||||

## RESULT 22

CS001427/c  
LOCUS  
DEFINITION 75 bp DNA linear SYN 01-FEB-2005  
Sequence 188 from Patent WO2005005462.  
ACCESSION CS001427  
VERSION CS001427.1 GI:58423905  
KEYWORDS  
SOURCE  
ORGANISM

synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Chan,A.C., Gordon,N.C., Kelley,R.F., Koehler,M.F. and Starovasinik,M.A.  
TITLE Blys antagonists and uses thereof  
JOURNAL Patent: WO 2005005462-A 20-JAN-2005;  
Genentech, Inc. (US)

## FEATURES

source  
1..75  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Clone 68"

## ORIGIN

Query Match 12.6%; Score 20.6; DB 11; Length 75;  
Best Local Similarity 62.7%; Pred. No. 1.8e+05;  
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3 TCGGCCACTTTGATGAGGGGACTGGGAGTCTTAGACAGTCCGAGTTC 53  
|||||  
DB 72 TCTTCACCGGTGATGAGGTGACAGGGCACCAGCGCGGACGAGGATC 22  
|||||

## RESULT 23

BOVB36/c  
LOCUS  
DEFINITION 60 bp mRNA linear MAM 14-DEC-2002  
Bos taurus mRNA for T-cell receptor beta chain, diversity and joining regions.

ACCESSION D90135  
VERSION D90135.1 GI:217465  
KEYWORDS  
SOURCE

ORGANISM

Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

AUTHORS Tanaka,A., Ishiguro,N. and Shinagawa,M.  
TITLE Sequence analysis of bovine T-cell receptor beta chain genes  
JOURNAL Unpublished  
COMMENT These data kindly submitted in computer readable form by: Atsuko Tanaka

Department of Veterinary Public Health  
Obihiro University of Agriculture and Veterinary Medicine  
Inada-cho  
Obihiro, Hokkaido 080

Phone: 81-155-48-5111 x281.  
Location/Qualifiers  
1..60  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="BVB36"  
/cell\_type="T cell"  
<1..>60  
/note="unnamed protein product; T-cell receptor beta chain, diversity region and joining region"

## FEATURES

source

## CDS

/translation="EADWGAARPDFGAGSWLTVV"

## ORIGIN

Query Match 12.4%; Score 20.4; DB 4; Length 60;  
Best Local Similarity 65.2%; Pred.No. 2.1e+05;  
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 107 CAGCCAGCTGCGGCCCGCCGAGTCAGGCGCGCTGCCCGCCAGTCC 6  
Db 51 CAGCCAGCTGCGGCCCGCCGAGTCAGGCGCGCTGCCCGCCAGTCC 6

## RESULT 24

CQ0561327 CQ0561327 65 bp DNA linear PAT 30-JAN-2004  
LOCUS  
DEFINITION Sequence 30962 from Patent WO0210449.  
ACCESSION CQ0561327  
VERSION CQ0561327.1 GI:41527754  
KEYWORDS  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
Patent: WO 0210449-A 30962 07-FEB-2002;  
CompuGen Inc. (US)

## FEATURES

source  
1..65  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

## ORIGIN

Query Match 12.4%; Score 20.4; DB 6; Length 65;  
Best Local Similarity 65.2%; Pred.No. 2.1e+05;  
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
QY 19 AGGGGAGCTGGGCGAGTCTTAGACAGTCCCGAAGTTCTCAAGGCACAG 64  
Db 6 AGGAGAGCTGAGCAGCTGGTCACAGTGCATCTGTGTCAGAGAACAG 51

## RESULT 25

CQ055775 CQ055775 77 bp DNA linear PAT 19-JAN-2004  
LOCUS  
DEFINITION Sequence 6595 from Patent WO0157270.  
ACCESSION CQ055775  
VERSION CQ055775.1 GI:41030281  
KEYWORDS  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.  
Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human breast and hbl 100 cells  
Patent: WO 0157270-A 6595 09-AUG-2001;

## JOURNAL

Aeonica, Inc. (US)  
NT HIT: AF110763.1, EVALUE 3.30e-02

## FEATURES

source  
1..77  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL033380.10  
EXPRESSED IN HBL100, SIGNAL = 1.3  
EST HUMAN HIT: W02144.1, EVALUE 3.60e+00  
NT HIT: AF110763.1, EVALUE 3.30e-02

SWISSPROT HIT: Q58016, EVALUE 5.40e+00"

## ORIGIN

Query Match 12.4%; Score 20.4; DB 6; Length 77;  
Best Local Similarity 61.1%; Pred.No. 2.1e+05;  
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 94 CGGGGAGGCGAGTGCAGCCAGCTGCAAGCCGCCACAGTGAAGAACATCTGAGCTCA 147  
Db 1 CTGGGAGACGGTGCAGCCAGATTCAAGCCAGGCTGCTGCTGGGATCA 54

Search completed: March 3, 2006, 08:38:47

Job time : 3435.27 secs



GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM nucleic - nucleic search, using sw model  
 Run on: March 3, 2006, 07:02:58 ; Search time 1070.86 Seconds  
 (without alignments)  
 1020.680 Million cell updates/sec  
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 Perfect score: 164  
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Scoring table: IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0  
 Searched: 4996997 seqs, 3332346308 residues  
 Total number of hits satisfying chosen parameters: 5180220  
 Minimum DB seq length: 0  
 Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

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 1: Geneseqn1980s.\*  
 2: Geneseqn1990s.\*  
 3: Geneseqn2000s.\*  
 4: Geneseqn2001as.\*  
 5: Geneseqn2001bs.\*  
 6: Geneseqn2002as.\*  
 7: Geneseqn2002bs.\*  
 8: Geneseqn2003as.\*  
 9: Geneseqn2003bs.\*  
 10: Geneseqn2003cs.\*  
 11: Geneseqn2003ds.\*  
 12: Geneseqn2004as.\*  
 13: Geneseqn2004bs.\*  
 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	16.5	75	6	AAL45878
2	27	16.5	75	6	ABL54799
3	25.4	15.5	75	6	AAL45879
4	25.4	15.5	75	6	ABL54800
5	23.6	14.4	65	6	ABN53195
6	22	13.4	65	6	ABN31002
7	21.8	13.3	78	3	AAV31802
8	21.8	13.3	78	3	AAA70677
9	21.8	13.3	78	6	AAD42076
10	21.8	13.3	78	10	AAD60100
11	21.8	13.3	78	10	ADH54440
12	21.8	13.3	78	13	ADU591414
13	21.8	13.3	78	13	ADT62543
14	21.8	13.3	78	13	ADU66735
15	21.4	13.0	65	6	ABN51533
16	21.2	12.9	65	6	ABN27744
17	21	12.8	21	2	AAQ79424
18	21	12.8	69	2	AAQ39611
19	21	12.8	69	2	AAQ62599

75	14	ADW21434	Adw21434 Blys bind
67	6	ABL75541	Ab175541 Corn tass
50	14	ADZ00380	Adz00380 Human gro
65	6	ABN11469	Abn11469 Rat splc
65	6	ABN55491	Abn55491 Mouse spl
75	14	ADW21450	Adw21450 Blys bind
65	6	ABN58214	Abn58214 Mouse spl
77	4	AAI20896	Aai20896 Probe #10
77	4	ABA65968	Ab65968 Human foe
77	4	AAI46135	Aai46135 Probe #14
77	4	ABA48083	Ab48083 Human bre
77	4	ABA33059	Ab33059 Probe #11
77	4	AAK40120	Aak40120 Human bon
77	4	AAK14390	Aak14390 Human bra
77	4	ABS39705	Ab39705 Human liv
77	5	AAI06604	Aai06604 Probe #65
77	6	ABS14187	Ab14187 Human gen
25	9	ACI20052	Ac120052 Human mic
50	5	ABL01077	Ab101077 Human SNP
60	6	ABN50504	Abn50504 Human spl
78	2	AAI17684	Aai17684 Recombina
78	2	AAI17668	Aai17668 Recombina
78	2	AAI17682	Aai17682 Recombina
80	2	AAI37014	Aai37014 Human cdc
80	2	AAI37051	Aai37051 Human cdc
34	13	ADT62814	Adt62814 Human alic
35	13	ADT62797	Adt62797 Human alic
35	13	ADT62809	Adt62809 Human alic
35	13	ADT62815	Adt62815 Human alic
36	13	ADT62816	Adt62816 Human alic
36	13	ADT62813	Adt62813 Human alic
36	13	ADT62808	Adt62808 Human alic
37	13	ADT62810	Adt62810 Human alic
37	13	ADT62807	Adt62807 Human alic
37	13	ADT62812	Adt62812 Human alic
51	4	AAI73944	Aai73944 Human sll
60	6	ABN47778	Abn47778 Human spl
60	6	ABN45286	Abn45286 Human spl
60	6	ABN45275	Abn45275 Human spl
50	4	AAI29364	Aai29364 Human SNP
41	10	ABZ57521	Abz57521 IGF bindi
41	10	ABZ57522	Abz57522 IGF bindi
60	6	ABN33297	Abn33297 Human spl
61	13	ADT02481	Adt02481 Recombina
70	4	AAF56802	Aaf56802 VEGF rece
78	14	ADZ45968	Adz45968 DNA enco
43	3	AAZ65121	Aaz65121 Probe spe
43	3	AAZ58245	Aaz58245 Human PRO
43	8	ACA64175	Ac64175 Novel hum
43	8	ABX80634	Abx80634 Human sec
43	8	ACD44143	Ac44143 Human PRO
43	8	ABX79314	Abx79314 Human sec
43	8	ACA93335	Ac93335 Secrete
43	8	ABX81017	Abx81017 Novel hum
43	8	ACA92833	Ac92833 Secrete
43	8	ABX16917	Abx16917 Human PRO
43	9	ACA67772	Ac67772 Novel hum
43	9	ACA88221	Ac88221 Human sec
43	9	ACD81728	Ac81728 Human PRO
43	9	ADA37545	Ad37545 Human sec
43	9	ADA21231	Ad21231 Human sec
43	9	ADA10018	Ad10018 Human PRO
43	9	ADA17562	Ad17562 Human PRO
43	9	ADA27670	Ad27670 Human sec
43	9	ADA94250	Ad94250 Human sec
43	9	ADA38475	Ad38475 Human sec
43	9	ADA92596	Ad92596 Human sec
43	9	ACH65289	Ac65289 Human sec
43	9	ADA22157	Ad22157 Human sec
43	9	ACD39279	Ac39279 Human PRO
43	9	ADA06323	Ad06323 Human sec
43	9	ADA39016	Ad39016 Human sec
43	9	ADB96042	Ad96042 Human PRO

93 19.4 11.8 43 10 ADC57514 Human PRO  
94 19.4 11.8 43 10 ADC54878 Human PRO  
95 19.4 11.8 43 10 ADC11745 Human sec  
96 19.4 11.8 43 10 ADC56167 Human PRO  
97 19.4 11.8 43 10 ADC07222 Human sec  
98 19.4 11.8 43 10 ADC11212 Human sec  
99 19.4 11.8 43 10 ADC14334 Secreted  
100 19.4 11.8 43 10 ADD07866 Human sec

## ALIGNMENTS

## RESULT 1

AA45878  
ID AAL45878 standard; DNA; 75 BP.  
XX AC  
XX AAL45878;  
XX AC  
DT 08-JUL-2002 (first entry)  
XX AC  
DE Modified acetylcholine receptor subunit alpha PCR primer #9.  
XX AC  
XX Insecticide; acetylcholine receptor; pharmaceutical; PCR; primer; ss.  
XX OS  
XX Synthetic.  
XX AC  
XX EP1184390-A2.  
XX AC  
PD 06-MAR-2002.  
XX AC  
PF 16-AUG-2001; 2001EP-00118963.  
XX AC  
PR 28-AUG-2000; 2000DE-01042177.  
XX AC  
PI (FARB ) BAYER AG.  
XX AC  
PI Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;  
XX AC  
DR WPI; 2002-271035/32.  
XX AC

New acetylcholine receptor subunit, useful for identifying plant-protection and therapeutic agents, comprises segment of insect subunit inserted into vertebrate subunit.  
XX AC  
XX Example 1; Page 43; 52pp; German.  
XX AC  
XX The present invention relates to a modified acetylcholine receptor in which at least one amino acid, in the region of an alpha-subunit of a vertebrate acetylcholine receptor that is homologous with a 45 amino acid sequence, is replaced by an amino acid that is present at the identical position in the corresponding region of an alpha-subunit of an insect acetylcholine receptor. This is useful for identifying new plant-protection agents and pharmaceuticals (for human or veterinary medicine), i.e. modulators of insect nicotinic receptors, for use as e.g. insecticides. The present sequence is a PCR primer for a modified acetylcholine receptor alpha subunit of the invention  
XX AC  
SQ Sequence 75 BP; 17 A; 20 C; 22 G; 16 T; 0 U; 0 Other;

Query Match 16.5%; Score 27; DB 6; Length 75;  
Best Local Similarity 60.0%; Pred. No. 60;  
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
Qy 18 GAGGGAGCTGGGCGAGTCTTAGACAGTCCCGAAGTTCTCAAGGCACAGGTCTCTTCCTGGT 77  
Db 1 GCGGGAGTGGGTCTATCTTAGAAGTCCCGCGCGTTCGACGAAAGTTTATACATGCT 60  
Qy 78 TTGACTGCTCTTACC 92  
Db 61 GCGACGAGCCCTACC 75

RESULT 3  
AAL45879/c  
ID AAL45879 standard; DNA; 75 BP.  
XX AC  
XX AAL45879;  
XX AC  
DT 08-JUL-2002 (first entry)  
XX AC

## RESULT 2

ABL54799  
ID ABL54799 standard; DNA; 75 BP.  
XX AC  
XX ABL54799;  
XX AC  
DT 13-JUN-2002 (first entry)  
XX AC  
DE Modified hen ACR subunit alpha 4 mutagenic oligo SEQ ID NO 16.  
XX AC  
XX Acetylcholine; receptor; ACR; subunit alpha; insect; insecticide; hen; plant-protection agent; veterinary; medicine; nicotinic receptor; ss.  
XX OS  
XX Synthetic.  
XX AC  
XX EP1184391-A2.  
XX AC  
PD 06-MAR-2002.  
XX AC  
PF 24-AUG-2001; 2001EP-00119704.  
XX AC  
PR 28-AUG-2000; 2000DE-01042177.  
XX AC  
PI (FARB ) BAYER AG.  
XX AC  
PI Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;  
XX AC  
DR WPI; 2002-271036/32.  
XX AC  
XX New acetylcholine receptor subunit, useful for identifying plant-protection and therapeutic agents, comprises a segment of insect subunit inserted into vertebrate subunit.  
XX AC  
XX Example 1; Page 10; 46pp; German.  
XX AC  
XX The invention relates to modified acetylcholine receptor (ACR) subunit (I) in which at least one amino acid (aa), in the region of an alpha-subunit of a vertebrate ACR that is homologous with a ACR of Torpedo californica (AB008882), is replaced by an aa that is present at the identical position in the corresponding region of an alpha-subunit of an insect ACR. (II), ACR containing them and the nucleic acid (II) encoding them, are useful for identifying new plant-protection agents and pharmaceuticals (for human or veterinary medicine), i.e. modulators (agonists or antagonists) of the properties of insect nicotinic receptors, e.g. insecticides. The present sequence is that of a mutagenic oligonucleotide used to generate the modified hen ACR alpha 4 subunit of the invention. The modified hen ACR alpha 4 subunit is generated by insertion of part of the nicotinic ACR alpha 1 subunit from the insect CC Heliothis virescens into the hen ACR alpha 4 subunit (Genbank AJ250361)  
XX AC  
SQ Sequence 75 BP; 17 A; 20 C; 22 G; 16 T; 0 U; 0 Other;

Query Match 16.5%; Score 27; DB 6; Length 75;  
Best Local Similarity 60.0%; Pred. No. 60;  
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
Qy 18 GAGGGAGCTGGGCGAGTCTTAGACAGTCCCGAAGTTCTCAAGGCACAGGTCTCTTCCTGGT 77  
Db 1 GCGGGAGTGGGTCTATCTTAGAAGTCCCGCGCGTTCGACGAAAGTTTATACATGCT 60  
Qy 78 TTGACTGCTCTTACC 92  
Db 61 GCGACGAGCCCTACC 75

RESULT 3  
AAL45879/c  
ID AAL45879 standard; DNA; 75 BP.  
XX AC  
XX AAL45879;  
XX AC  
DT 08-JUL-2002 (first entry)  
XX AC

DE	Modified acetylcholine receptor subunit alpha PCR primer #10.
XX	
KW	Insecticide; acetylcholine receptor; pharmaceutical; PCR; primer; ss.
XX	
OS	Synthetic.
XX	
PN	EP1184390-A2.
XX	
PD	06-MAR-2002.
XX	
XX	
XX	16-AUG-2001; 2001EP-00118863.
PF	
XX	
PR	28-AUG-2000; 2000DE-01042177.
XX	
XX	(FARB ) BAYER AG.
XX	
PI	Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;
XX	
XX	WPI; 2002-271035/32.
XX	
PT	New acetylcholine receptor subunit, useful for identifying plant-
PT	protection and therapeutic agents, comprises segment of insect subunit
PT	inserted into vertebrate subunit.
XX	
XX	Example 1; Page 44; 52pp; German.
XX	
CC	The present invention relates to a modified acetylcholine receptor in
CC	which at least one amino acid, in the region of an alpha-subunit of a
CC	vertebrate acetylcholine receptor that is homologous with a 45 amino acid
CC	sequence, is replaced by an amino acid that is present at the identical
CC	position in the corresponding region of an alpha-subunit of an insect
CC	acetylcholine receptor. This is useful for identifying new plant-
CC	protection agents and pharmaceuticals (for human or veterinary medicine),
CC	i.e. modulators of insect nicotinic receptors, for use as e.g.
CC	insecticides. The present sequence is a PCR primer for a modified
CC	acetylcholine receptor alpha subunit of the invention
XX	
SQ	Sequence 75 BP; 16 A; 22 C; 20 G; 17 T; 0 U; 0 Other;
	Query Match 15.5%; Score 25.4; DB 6; Length 75;
	Best Local Similarity 58.7%; Pred. No. 2.1e+02;
	Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY	18 GAGGGGACTGGGCGAGTTCTAGACAGTCCCGAAAGTTCTCAAGGCACAGTCTCTTCTCGTGT 77
Db	
	75 GCGGGGAGTGGTGCATCATTTGAAGTCCGGCCGTTGCGACGAAAGTTTATACATGCT 16
QY	78 TTGACTGTCTCTTACC 92
Db	
	15 GCGACGAGCCCTACC 1
	RESULT 4
	ABL54800/c
ID	ABL54800 standard; DNA; 75 BP.
XX	
AC	ABL54800;
XX	
DT	13-JUN-2002 (first entry)
XX	
DE	Modified hen ACR subunit alpha 4 mutagenic oligo SEQ ID NO 17.
XX	
KW	Acetylcholine; receptor; ACR; subunit alpha; insect; insecticide; hen;
KW	plant-protection agent; veterinary; medicine; nicotinic receptor; ss.
XX	
OS	Synthetic.
XX	
XX	EP1184391-A2.
PN	
XX	
PD	06-MAR-2002.
XX	
XX	
XX	24-AUG-2001; 2001EP-00119704.
PF	
XX	

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PR 28-AUG-2000; 2000DE-01042177.
XX
XX (FARB ) BAYER AG.
XX
XX Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;
XX
XX WPI; 2002-271036/32.
XX
XX New acetylcholine receptor subunit, useful for identifying plant-
PT protection and therapeutic agents, comprises a segment of insect subunit
PT inserted into vertebrate subunit.
XX
XX Example 1; Page 10; 46pp; German.
XX
XX The invention relates to modified acetylcholine receptor (ACR) subunit
CC (I) in which at least one amino acid (aa), in the region of an alpha-
CC subunit of a vertebrate ACR that is homologous with a ACR of Torpedo
CC californica (ABB08882), is replaced by an aa that is present at the
CC identical position in the corresponding region of an alpha-subunit of an
CC insect ACR. (I), ACR containing them and the nucleic acid (II) encoding
CC them, are useful for identifying new plant-protection agents and
CC pharmaceuticals (for human or veterinary medicine), i.e. modulators
CC (agonists or antagonists) of the properties of insect nicotinic
CC receptors, e.g. insecticides. The present sequence is that of a mutagenic
CC oligonucleotide used to generate the modified hen ACR alpha 4 subunit of
CC the invention. The modified hen ACR alpha 4 subunit is generated by
CC insertion of part of the nicotinic ACR alpha 1 subunit from the insect
CC Heliothis virescens into the hen ACR alpha 4 subunit (Genbank AJ250361)
XX
XX Sequence 75 BP; 16 A; 22 C; 20 G; 17 T; 0 U; 0 Other;
SQ
Query Match 15.5%; Score 25.4; DB 6; Length 75;
Best Local Similarity 58.7%; Pred.No. 2.1e+02;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 18 GAGGGGACTGGGCGAGTTCTAGACAGTCCCGAAGTTCTCAAGGCACAGGTCTCTTCCTGGT 77
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
75 GCGGGGAGTGGGTGCATCTGAAGTCCGCGCCGTTGCGAACGAAAGTTTTATACATGCT 16
QY 78 TTGACTGTCTTACC 92
Db ||| ||||| |||||
15 GCGACGAGCCCTACC 1
RESULT 5
ABN53195
ID ABN53195 standard; DNA; 65 BP.
XX
XX ABN53195;
XX
XX 15-JUL-2002 (first entry)
XX
XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:25943.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Mus musculus.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB001903.
XX
XX 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX

```

XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
XX Example 1; SEQ ID NO 25943; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 65 BP; 15 A; 17 C; 16 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 14.4%; Score 23.6; DB 6; Length 65;  
Best Local Similarity 61.3%; Pred. No. 7.9e+02;  
Matches 38; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 3 TCGGCCACCTTGTAGAGGGAGCTGGGCGAGTCTTAGACAGTCCGAGTTCTCAAGGCAC 62  
DB 3 TCGGCCAACTGTGTAGTCAGTAATGCCTGTTCAACTGAGGCTGTATCAAACTCTGGCAC 62  
QY 63 AG 64  
DB 63 AG 64  
RESULT 6  
ABN31002/c  
ID AEN31002 standard; DNA; 65 BP.  
XX AEN31002;  
XX  
XX 15-JUL-2002 (first entry)  
XX  
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:3750.  
XX  
XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Rattus norvegicus.  
XX  
XX WO200210449-A2.  
XX  
XX 07-FEB-2002.  
XX  
XX 20-JUL-2001; 2001WO-IB001903.  
XX  
XX 28-JUL-2000; 2000US-0221607P.  
XX  
XX 02-MAY-2001; 2001US-0287724P.  
XX  
XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WPI; 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
XX Example 1; SEQ ID NO 3750; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcripts. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 65 BP; 18 A; 23 C; 12 G; 12 T; 0 U; 0 Other;  
SQ  
Query Match 13.4%; Score 22; DB 6; Length 65;  
Best Local Similarity 59.7%; Pred. No. 2.7e+03;  
Matches 37; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 17 TGAAGGGAGCTGGGCGAGTCTTAGACAGTCCGAGTTCTCAAGGCACAGGTCTCTCTGG 76  
DB 64 TGGGAGGAGTCTGAGGTCTCTGAATTCGAAATTCGAAATTCGAGCGAGGTGCTGCTGG 5  
QY 77 TT 78  
DB 4 GT 3  
RESULT 7  
AAV31802  
ID AAV31802 standard; DNA; 78 BP.  
XX AAV31802;  
XX  
XX 21-AUG-1998 (first entry)  
XX  
XX Human growth hormone signal peptide nucleotide sequence.  
XX  
XX Human alpha-galactosidase A gene; alpha-gal A gene; X-linked;  
XX glycosylated human alpha-gal A; Fabry disease; alpha-gal A deficiency;  
XX lysosomal storage disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9811206-A2.  
XX  
XX 19-MAR-1998.  
XX  
XX 12-SEP-1997; 97WO-US016603.  
XX  
XX 13-SEP-1996; 96US-00712614.  
XX

XX PA (TRAN-) TRANSKARYOTIC THERAPIES INC.  
XX Selden RF, Borowski M, Gillespie FP, Kinoshita CM, Treco DA;  
PI Williams MD;  
XX WPI: 1998-207375/18.  
XX P-PSDB; AAB37989.  
XX Treatment of alpha-galactosidase A deficiency in, e.g. Fabry disease -  
PT comprises use of genetically modified human cells that express alpha-  
PT galactosidase.  
XX Disclosure; Fig 11; 78pp; English.  
XX This is the nucleotide sequence of the human growth hormone signal  
CC peptide, used in the method of the invention, which involves the  
CC production of genetically modified human cells that express alpha-  
CC galactosidase. The cultured human cells can be used for the production of  
CC glycosylated human alpha-gal A and can be used for the treatment of  
CC patients with an alpha-gal A deficiency, e.g. Fabry disease (an X-linked  
CC inherited lysosomal storage disease)  
XX Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;  
SQ Query Match 13.3%; Score 21.8; DB 2; Length 78;  
Best Local Similarity 56.2%; Pred. No. 3.4e+03;  
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 35 CTAGACAGTCCCGAGTCTCTCAAGGCACACAGGTCTCTCTGCTTTGACGTGCTTACCCC 94  
Db 5 CTACAGGCTCCCGAGCTCCCTGCTCTGCTTTGGCTGCTGCTGCTGCTGCTGCTGCTTC 64  
QY 95 GGGAGGCAGTGC 107  
Db 65 AAGAGGCAGTGC 77  
RESULT 8  
AAA70677  
ID AAA70677 standard; DNA; 78 BP.  
XX AC AAA70677;  
XX 15-DEC-2000 (first entry)  
XX Human growth hormone signal peptide coding sequence.  
XX Nephrotropic; gene therapy; alpha-galactosidase A deficiency; sg;  
KW Fabry disease; secretion; human growth hormone; hGH; signal peptide;  
KW enzyme replacement therapy.  
XX Homo sapiens.  
XX US6083725-A.  
XX 04-JUL-2000.  
XX 12-SEP-1997; 97US-00928881.  
XX 13-SEP-1996; 96US-0026041P.  
XX (TRAN-) TRANSKARYOTIC THERAPIES INC.  
XX Kinoshita CM, Treco DA, Williams MD, Selden RF, Borowski M;  
PI Gillespie FP;  
XX WPI: 2000-464341/40.  
XX P-PSDB; AAB15386.  
XX New DNA comprising a human growth hormone signal peptide and human alpha-  
PT galactosidase A polypeptide and cells expressing the DNA, useful for  
PT treating Fabry disease and in vitro protein production for enzyme

PT replacement therapy.  
XX Disclosure; Fig 11; 32pp; English.  
XX The invention relates to the treatment of a patient having an alpha-  
CC galactosidase A (AGA) deficiency, e.g. Fabry disease, by using cells  
CC overexpressing and secreting AGA or purified AGA. This sequence  
CC corresponds to the human growth hormone (hGH) signal peptide which is  
CC fused to the N-terminal of the AGA protein for secretion. Primary,  
CC secondary, or immortalised human cells genetically modified to  
CC overexpress human AGA are also useful for in vitro protein production, to  
CC produce protein which may be purified for enzyme replacement therapy. The  
CC method allows the production of large quantities of appropriately  
CC glycosylated and therapeutically useful human AGA  
XX Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;  
SQ Query Match 13.3%; Score 21.8; DB 3; Length 78;  
Best Local Similarity 56.2%; Pred. No. 3.4e+03;  
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 35 CTAGACAGTCCCGAGTCTCTCAAGGCACACAGGTCTCTCTGCTTTGACGTGCTTACCCC 94  
Db 5 CTACAGGCTCCCGAGCTCCCTGCTCTGCTTTGGCTGCTGCTGCTGCTGCTGCTTC 64  
QY 95 GGGAGGCAGTGC 107  
Db 65 AAGAGGCAGTGC 77  
RESULT 9  
AAD42076  
ID AAD42076 standard; DNA; 78 BP.  
XX AC AAD42076;  
XX 04-NOV-2002 (first entry)  
XX Human growth hormone (hGH) signal peptide encoding DNA.  
XX Human; alpha-galactosidase A; alpha-gal A deficiency; Fabry disease;  
KW enzyme; growth hormone; hGH signal peptide; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 1..78  
FT /\*tag= a  
FT /\*product= "hGH signal peptide"  
FT /\*note= "No stop codon"  
FT /\*partial  
XX US6395884-B1.  
XX 28-MAY-2002.  
XX 06-APR-2000; 2000US-00543921.  
XX 13-SEP-1996; 96US-0026041P.  
XX 12-SEP-1997; 97US-00928881.  
XX (TRAN-) TRANSKARYOTIC THERAPIES INC.  
XX Selden RF, Borowski M, Gillespie FP, Kinoshita CM, Treco DA;  
PI Williams MD;  
XX WPI: 2002-526374/56.  
XX P-PSDB; AAE24539.  
XX Purifying human alpha-galactosidase A from a cell for use in treating  
PT Fabry disease, by passing sample containing the enzyme over hydrophobic  
PT interaction resin, heparin resin, hydroxyapatite and anion exchange  
PT resin.

XX PS Disclosure; Col 33-34; 31pp; English.  
 CC The invention relates to a method of purifying human alpha-galactosidase  
 CC A (alpha-gal A) from a human cell. The method involves a chromatography  
 CC step which comprises passing human alpha-gal A containing sample over a  
 CC hydrophobic interaction resin. The method is useful for purifying alpha-  
 CC gal A from a human cell, for use in treating an individual suspected of  
 CC having alpha-gal A deficiency such as Fabry disease. The present sequence  
 CC is human growth hormone (hGH) signal peptide encoding DNA. This sequence  
 CC is used to illustrate the method of the invention  
 XX  
 SQ Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 13.3%; Score 21.8; DB 6; Length 78;  
 Best Local Similarity 56.2%; Pred. No. 3.4e+03;  
 Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 35 CTAGACAGTCCCGAAGTCTCAAGGCACAGTCTCTTCTGGTTTGTACTGTCTCTTACCCC 94  
 Db 5 CTACAGGCTCCCGAGCTCCTGCTCTGCTTTTGGCCCTGCTGCTGCTGCTGCTGCTGCTC 64  
 QY 95 GGGGAGGCGAGTGC 107  
 Db 65 AAGAGGGCGAGTGC 77

RESULT 10  
 AAD60100  
 ID AAD60100 standard; DNA; 78 BP.  
 AC AAD60100;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE hGH signal peptide DNA (without intron).  
 XX  
 KW Human growth hormone; glucocerebrosidase; gene therapy; cardiovascular;  
 KW Gaucher's disease; Fabry disease; alpha-galactosidase A deficiency; hGH;  
 KW CNS; nephrotropic; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6566099-B1.  
 XX  
 PD 20-MAY-2003.  
 XX  
 PF 27-JAN-2000; 2000US-00491759.  
 XX  
 PR 13-SEP-1996; 96US-0026041P.  
 PR 12-SEP-1997; 97US-00928881.  
 XX  
 PA (TRAN-) TRANSKARYOTIC THERAPIES INC.  
 XX  
 PI Selden RF, Borowski M, Gillispie FP, Kinoshita CM, Treco DA;  
 PI Williams MD;  
 XX  
 DR WPI; 2003-719643/68.  
 XX  
 PT Novel polypeptide comprising signal peptide of human growth hormone  
 PT linked to glucocerebrosidase useful for treating disorders associated  
 PT with enzyme deficiency in sphingolipid degradation such as Gaucher  
 PT disease.  
 XX  
 PS Disclosure; Fig 11; 30pp; English.  
 CC The present invention relates to a novel polypeptide comprising signal  
 CC peptide of human growth hormone (hGH) linked to glucocerebrosidase. The  
 CC invention is useful for treating disorders associated with alpha-  
 CC galactosidase A deficiency and sphingolipid degradation such as Gaucher's  
 CC disease and Fabry disease. The invention is also useful in gene therapy.  
 CC The present sequence is hGH signal peptide DNA (without intron)  
 XX

SQ Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;  
 Query Match 13.3%; Score 21.8; DB 10; Length 78;  
 Best Local Similarity 56.2%; Pred. No. 3.4e+03;  
 Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 35 CTAGACAGTCCCGAAGTCTCAAGGCACAGTCTCTTCTGGTTTGTACTGTCTCTTACCCC 94  
 Db 5 CTACAGGCTCCCGAGCTCCTGCTCTGCTTTTGGCCCTGCTGCTGCTGCTGCTGCTGCTC 64  
 QY 95 GGGGAGGCGAGTGC 107  
 Db 65 AAGAGGGCGAGTGC 77

RESULT 11  
 ADH54440  
 ID ADH54440 standard; DNA; 78 BP.  
 AC ADH54440;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Human GH (growth hormone) signal peptide DNA.  
 XX  
 KW Alpha-galactosidase A; nephrotropic; gene therapy; Fabry disease; human;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key  
 FT CDS  
 FT Location/Qualifiers  
 FT 1..78  
 FT /\*tag= a  
 FT /product= "Human growth hormone signal peptide"  
 FT /partial  
 FT /note= "No stop codon"  
 XX  
 PN US2003152560-A1.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 12-DEC-2002; 2002US-00318905.  
 XX  
 PR 13-SEP-1996; 96US-0026041P.  
 PR 12-SEP-1997; 97US-00928881.  
 PR 27-JAN-2000; 2000US-00491759.  
 XX  
 PA (TRAN-) TRANSKARYOTIC THERAPIES INC.  
 XX  
 PI Selden RF, Borowski M, Gillispie FP, Kinoshita CM, Treco DA;  
 PI Williams MD;  
 XX  
 DR WPI; 2003-897682/82.  
 DR P-PSDB; ADH54439.  
 XX  
 PT Therapeutic method in alpha-galactosidase A deficiency using genetically  
 PT modified cells overexpressing and secreting the human alpha-galactosidase  
 PT A, useful particularly for treating Fabry disease.  
 XX  
 PS Disclosure; SEQ ID NO 22; 33pp; English.  
 CC The invention relates to a method of treatment which comprises  
 CC identifying a patient suspected of having an alpha-galactosidase A  
 CC deficiency, and introducing into the patient a human cell genetically  
 CC modified to overexpress and secrete human alpha-gal A. The invention is  
 CC useful in gene therapy. The methods and compositions of the present  
 CC invention are useful for treating disorders with alpha-galactosidase  
 CC deficiency, such as Fabry disease. The present sequence is human growth  
 CC hormone signal peptide DNA used in the amplification of the invention.  
 XX  
 SQ Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;  
 Query Match 13.3%; Score 21.8; DB 10; Length 78;



PA (LOU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.  
 XX Cooper RK, Fioretti WC, Cadd GG;  
 XX WPI; 2004-581003/56.  
 XX  
 XX New polynucleotide (transposon-based vector) cassette comprising gene of  
 PT interest operably linked to a cecropin prepro sequence, is useful in  
 PT producing vaccines to protect an individual against infectious diseases.  
 XX  
 XX Disclosure; SEQ ID NO 28; 155pp; English.  
 XX  
 XX The patent discloses novel, effective and efficient method of producing  
 CC multimeric proteins, antibodies using transposon-based vectors, in  
 CC transgenic individuals. These proteins can be used as a vaccine.  
 CC Immunising individuals with such compositions, comprising vaccines is  
 CC capable of generating an immune response, to prevent or ameliorate the  
 CC severity of a disease. The invention provides polynucleotide cassettes  
 CC containing at least one gene of interest and one or more pro  
 CC polynucleotide sequence, where in each gene of interest are operably-  
 CC linked to a pro nucleotide sequence of at least one gene of interest. The  
 CC transposon-based vector comprises the polynucleotide and further  
 CC comprises a transposase gene operably linked to a first promoter and  
 CC where the first promoter comprises a modified Kozak sequence, two or more  
 CC genes of interest are each operably-linked to one or more additional  
 CC promoters, and two or more genes of interest and their operably-linked  
 CC promoters are flanked by transposase insertion sequences recognized by a  
 CC transposase encoded by the transposase gene. Many diseases and disease  
 CC causing organisms can be targets of the vaccine of the present invention.  
 CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,  
 CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus  
 CC fever, viral hemorrhagic fever, etc. The preferred animal for production  
 CC of protein is a bird or a mammal. The egg or milk of these animals  
 CC comprises the multimeric protein encoded by the isolated polynucleotide  
 CC of the invention. Hence, these proteins are endowed with varied  
 CC properties and are antibacterial, anti viral, antimicrobial, anti-  
 CC inflammatory, and neuroprotective in nature. The sequence presented here  
 CC is the polynucleotide encoding signal peptide sequence.  
 XX  
 XX Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;  
 SQ  
 Query Match 13.3%; Score 21.8; DB 13; Length 78;  
 Best Local Similarity 56.2%; Pred. No. 3.4e+03;  
 Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 35 CTAGACAGTCCGAGTCTCTCAGGCACAGGTCTCTCTGTTGACTGCTTACCTACCCC 94  
 DB 5 CTACAGGCTCCGAGCTCCCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTC 64  
 QY 95 GGGGAGGCACTGC 107  
 DB 65 AAGAGGGCAGTGC 77  
 RESULT 14  
 ADU66735  
 ID ADU66735 standard; DNA; 78 BP.  
 XX  
 AC ADU66735;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Signal peptide encoding polynucleotide, seqid:28.  
 XX  
 XX Multimeric protein; transgenic; leukaemia inhibitory factor;  
 KW tumour necrosis factor; angiotensin; bone morphogenetic protein;  
 KW adrenomedullin; calcitonin; amyloid; calcitonin gene-related peptide;  
 KW insulin; growth hormone releasing hormone; GHRH;  
 KW granulocyte-macrophage colony stimulating factor; G-CSF; albumin;  
 KW apolipoprotein; anti-hepatitis antibody; anti-cytomegalovirus antibody;  
 KW anti-rabies antibody; antivenin latrodectus; thyrotropin;  
 KW glial cell line-derived neurotrophic factor;  
 KW antineoplastic cancer antibody; ss.

XX Unidentified.  
 OS  
 XX US2004235011-A1.  
 PN  
 XX 25-NOV-2004.  
 PD  
 XX  
 XX 24-DEC-2003; 2003US-00746943.  
 PF  
 XX  
 XX 26-JUN-2002; 2002US-0392415P.  
 PR 21-JAN-2003; 2003US-0441377P.  
 PR 21-JAN-2003; 2003US-0441381P.  
 PR 21-JAN-2003; 2003US-0441392P.  
 PR 21-JAN-2003; 2003US-0441405P.  
 PR 21-JAN-2003; 2003US-0441477P.  
 PR 21-JAN-2003; 2003US-0441502P.  
 PR 26-JUN-2003; 2003US-00609019.  
 XX  
 XX (COOP/) COOPER R K.  
 PA (FIOR/) FIORETTI W C.  
 PA (CADD/) CADD G G.  
 XX  
 XX Cooper RK, Fioretti WC, Cadd GG;  
 PI  
 XX WPI; 2004-832941/82.  
 DR  
 XX  
 XX Novel isolated polynucleotide comprising genes of interest e.g., anti-  
 PT her2, and pro nucleotide sequences, useful for producing multimeric  
 PT proteins such as antineoplastic cancer antibodies, in animals.  
 XX  
 PS Disclosure; SEQ ID NO 28; 107pp; English.  
 XX  
 CC The invention relates to a polynucleotide sequence comprising genes of  
 CC interest and pro nucleotide sequences. The invention also relates to a  
 CC method for producing multimeric protein or multivalent multimeric  
 CC protein. The polynucleotide sequence of the invention is useful for  
 CC producing multimeric proteins in a transgenic individual such as egg-  
 CC laying animal or a milk-producing animal. It is useful in producing  
 CC multimeric proteins or proteins such as leukaemia inhibitory factor,  
 CC tumour necrosis factor alpha and beta, angiotensin, bone morphogenetic  
 CC proteins, adrenomedullin, calcitonin, amyloid, calcitonin gene-related  
 CC peptide, insulin, growth hormone releasing hormone (GHRH), granulocyte-  
 CC macrophage colony stimulating factor (G-CSF), albumin, apolipoprotein,  
 CC anti-hepatitis antibody, anti-cytomegalovirus antibody, anti-rabies  
 CC antibody, antivenin latrodectus, thyrotropin, glial cell line-derived  
 CC neurotrophic factor, antineoplastic cancer antibody etc. The present  
 CC sequence is a signal peptide encoding polynucleotide. This sequence is  
 CC used in the production of multimeric proteins.  
 XX  
 SQ Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;  
 Query Match 13.3%; Score 21.8; DB 13; Length 78;  
 Best Local Similarity 56.2%; Pred. No. 3.4e+03;  
 Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 35 CTAGACAGTCCGAGTCTCTCAGGCACAGGTCTCTCTGTTGACTGCTTACCTACCCC 94  
 DB 5 CTACAGGCTCCGAGCTCCCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTC 64  
 QY 95 GGGGAGGCACTGC 107  
 DB 65 AAGAGGGCAGTGC 77  
 RESULT 15  
 ABN51533  
 ID ABN51533 standard; DNA; 65 BP.  
 XX  
 AC ABN51533;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:24281.



XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX Mus musculus.  
XX WO200210449-A2.  
XX 07-FEB-2002.  
XX 20-JUL-2001; 2001WO-IB001903.  
XX 28-JUL-2000; 2000US-0221607P.  
XX 02-MAY-2001; 2001US-0287724P.  
XX (COMP-) COMPUGEN INC.  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WPI; 2002-257383/30.  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX Example 1; SEQ ID NO 24281; 47pp; English.  
XX The present invention describes oligonucleotide libraries for detecting  
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
XX )transcriptome comprises messenger RNAs transcribed from multiple  
XX transcription units that populate a genome. The library comprises several  
XX oligonucleotides, each capable of hybridizing selectively to a set of  
XX messenger RNAs transcribed from a given transcription unit of the genome,  
XX which encodes one or more messenger RNA splice variants. The  
XX oligonucleotide libraries are useful for detecting mRNAs from a  
XX biological sample, in expression profiling studies, in qualitatively or  
XX quantitatively characterizing the corresponding transcriptome, and in  
XX detecting RNA transcripts and splice variants of human or animal  
XX transcriptomes. The libraries may also be used as specialised mini  
XX libraries to detect transcripts of a sub-transcriptome under a particular  
XX biological or pathological state, and so allowing the detection of tissue  
XX - and pathology-specific genes such as those genes only expressed in  
XX specific tissue under a specific pathological condition; to detect  
XX developmental specific genes; and to detect RNA transcripts and splice  
XX variants of a transcriptome of a patient suffering from a particular  
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
XX rats, humans and mice, which are used in the exemplification of the  
XX present invention. N.B. The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 65 BP; 23 A; 12 C; 20 G; 10 T; 0 U; 0 Other;  
Query Match 13.0%; Score 21.4; DB 6; Length 65;  
Best Local Similarity 61.8%; Pred. No. 4.4e+03;  
Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
\*QY 89 TACCCGGGAGCAGTCGAGCCAGTCGACAGCCCGACAGTCGACAGTCGAG 143  
DB 8 TACAGGTGGAGTTGTGAAGCAAACTGAACCTGCGGCATTAAAGGCCATCGGAG 62  
RESULT 16  
ABN27744/C  
ID ABN27744 standard; DNA; 65 BP.  
XX AC  
XX ABN27744;  
XX 15-JUL-2002 (first entry)  
XX DT  
XX DE Rat spliced transcript detection oligonucleotide SEQ ID NO:492.  
XX

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX Rattus norvegicus.  
XX WO200210449-A2.  
XX 07-FEB-2002.  
XX 20-JUL-2001; 2001WO-IB001903.  
XX 28-JUL-2000; 2000US-0221607P.  
XX 02-MAY-2001; 2001US-0287724P.  
XX (COMP-) COMPUGEN INC.  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WPI; 2002-257383/30.  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX Example 1; SEQ ID NO 492; 47pp; English.  
XX The present invention describes oligonucleotide libraries for detecting  
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
XX )transcriptome comprises messenger RNAs transcribed from multiple  
XX transcription units that populate a genome. The library comprises several  
XX oligonucleotides, each capable of hybridizing selectively to a set of  
XX messenger RNAs transcribed from a given transcription unit of the genome,  
XX which encodes one or more messenger RNA splice variants. The  
XX oligonucleotide libraries are useful for detecting mRNAs from a  
XX biological sample, in expression profiling studies, in qualitatively or  
XX quantitatively characterizing the corresponding transcriptome, and in  
XX detecting RNA transcripts and splice variants of human or animal  
XX transcriptomes. The libraries may also be used as specialised mini  
XX libraries to detect transcripts of a sub-transcriptome under a particular  
XX biological or pathological state, and so allowing the detection of tissue  
XX - and pathology-specific genes such as those genes only expressed in  
XX specific tissue under a specific pathological condition; to detect  
XX developmental specific genes; and to detect RNA transcripts and splice  
XX variants of a transcriptome of a patient suffering from a particular  
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
XX rats, humans and mice, which are used in the exemplification of the  
XX present invention. N.B. The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 65 BP; 28 A; 9 C; 20 G; 8 T; 0 U; 0 Other;  
Query Match 12.9%; Score 21.2; DB 6; Length 65;  
Best Local Similarity 69.0%; Pred. No. 5.1e+03;  
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 58 GGCAGAGTCCTCTCTGCTTGTGACTGTCTTACCCCGGGA 99  
DB 42 GTCACTGTGCTTCTTGTGTAATCTGTCTTAACCCCTTGTA 1  
RESULT 17  
AAQ79424  
ID AAQ79424 standard; DNA; 21 BP.  
XX AC  
XX AAQ79424;  
XX 25-MAR-2003 (revised)  
XX DT 03-JUN-1995 (first entry)  
XX DE PCR primer no. 12 based on human hepatocyte inducible nitric oxide  
XX synthase (iNOS) cDNA.







CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 65 BP; 20 A; 16 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 12.6%; Score 20.6; DB 6; Length 65;  
 Best Local Similarity 62.7%; Pred. No. 8.1e+03;  
 Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 40 CAGTCCCGAGTCTTCAAGCAGACAGTCTCTTCTGTTGACTGTCCTTA 90  
 |||||  
 DB 6 CAGTGAAGCAGATCTTCAGACAGACAGACTCACTCTCTAGGAACTCTCA 56  
 |||||

RESULT 24  
 ABN55491  
 ID ABN55491 standard; DNA; 65 BP.  
 XX  
 AC ABN55491;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28239.  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-1B001903.  
 XX  
 PR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 28239; 47pp; English.  
 XX  
 PS The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 65 BP; 22 A; 14 C; 17 G; 12 T; 0 U; 0 Other;

Query Match 12.6%; Score 20.6; DB 6; Length 65;  
 Best Local Similarity 67.4%; Pred. No. 8.1e+03;  
 Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 97 GCAGGCGAGTCCAGCGCTGCAAGCCCCACAGTGAAGAACATC 139  
 |||||  
 DB 10 GGTGCACACTGAAGCTGTTGAAGACACCAGTGAAGAACTTC 52  
 |||||

RESULT 25  
 ADW21450/c  
 ID ADW21450 standard; DNA; 75 BP.  
 XX  
 AC ADW21450;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE Blys binding-peptide, encoding DNA, SEQ ID 188.  
 XX  
 KW Blys; B lymphocyte stimulator; B lymphocyte stimulator antagonist;  
 KW immune disorder; cancer; cytostatic; neoplasm; rheumatoid arthritis;  
 KW multiple sclerosis; systemic lupus erythematosus; phage display;  
 KW Antirheumatic; Antiarthritis; Neuroprotective; Antiinflammatory;  
 KW Dermatological; Immunosuppressive; leukemia; lymphoma; myeloma; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005005462-A2.  
 XX  
 PD 20-JAN-2005.  
 XX  
 PF 04-JUN-2004; 2004WO-US017682.  
 XX  
 PR 05-JUN-2003; 2003US-0476414P.  
 PR 05-JUN-2003; 2003US-0476481P.  
 PR 06-JUN-2003; 2003US-0476531P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chan AC, Gordon NC, Kelley RF, Koehler MFT, Starovasnik MA;  
 XX  
 DR WPI; 2005-092059/10.  
 DR P-PSDB; ADW21372.  
 XX  
 PT New polypeptide or Blys antagonist, for treating an immune-related  
 PT condition (e.g. rheumatoid arthritis, multiple sclerosis or systemic  
 PT lupus erythematosus) or cancer (e.g. leukemia or lymphoma).  
 XX  
 PS Example 2; SEQ ID NO 188; 226pp; English.

CC The invention relates to a polypeptide comprising sequences of formula I,  
 CC II or III, (detailed in the claims) which are antagonists of BlyS (B cell  
 CC stimulator). Also included are a nucleic acid molecule encoding the  
 CC polypeptide, a vector comprising the nucleic acid molecule, a host cell  
 CC comprising the nucleic acid molecule, a method for producing a  
 CC polypeptide, a composition comprising the polypeptide optionally further  
 CC comprising a physiological carrier, a method for detecting an inhibitor  
 CC of BlyS binding to BR3 (BlyS receptor 3) in vitro, a method for  
 CC inhibiting BlyS binding to BR3 in a mammal, a method for inhibiting BlyS  
 CC signaling in a mammal and a method for treating an immune-related  
 CC condition or cancer in a mammal. The sequence of Formula I, II or III is  
 CC a sequence fused or conjugated to an immunoadhesion protein or to an  
 CC antibody, where the antibody is a F(ab) antibody, F(ab')<sub>2</sub> antibody, a  
 CC scfv antibody, a humanized antibody or multispecific antibody, e.g., a  
 CC antibodies directed against CD20. The polypeptide is conjugated to an  
 CC agent, e.g. a growth inhibitory agent, a cytotoxic agent, a detection  
 CC agent, an agent that improves the bioavailability of the polypeptide and  
 CC an agent that improves the half-life of the polypeptide, where the  
 CC cytotoxic agent is a toxin, an antibiotic or a radioactive isotope. The  
 CC polypeptide, composition and methods are useful for treating an immune-  
 CC related condition (many examples given in the specification), e.g.  
 CC rheumatoid arthritis, multiple sclerosis or systemic lupus erythematosus  
 CC or for treating cancer (many examples given in the specification), e.g.  
 CC leukemia, lymphoma or myeloma. The peptides were isolated from a phage  
 CC display library, where the DNAs encoding them additionally encoded a  
 CC peptide linker and an STII signal peptide. The present sequence is a DNA  
 CC encoding a BlyS-binding peptide of the invention.

SQ Sequence 75 BP; 12 A; 24 C; 20 G; 19 T; 0 U; 0 Other;

Query Match 12.6%; Score 20.6; DB 14; Length 75;  
 Best Local Similarity 62.7%; Pred. No. 8.5e+03;  
 Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 3 TCGGCCACCTTTGATGAGGGGACTGGCCAGTCTTAGACAGTCCCGAAGTTC 53  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 72 TCCTCCACCGGTGATGAGGTGACAGGGCACCCAGCGCGAACCAGGAGATC 22

Search completed: March 3, 2006, 08:00:13  
 Job time : 1077.86 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 215.424 Seconds  
 (without alignments)  
 1353.240 Million cell updates/sec

Title: US-10-655-801-3\_COPY\_14\_177  
 Perfect score: 164  
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Scoring table: IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0  
 Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

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 3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
 4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
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 6: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq.\*  
 7: /cgn2\_6/prodata/1/ina/PF COMB.seq.\*  
 8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
 9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	13.3	78	3	US-08-928-881-22
2	21.8	13.3	78	3	US-09-543-921-22
3	21.8	13.3	78	3	US-09-491-759-22
4	20.2	12.3	78	2	US-08-089-974B-4
5	20.2	12.3	78	2	US-08-089-974B-18
6	20.2	12.3	78	2	US-08-089-974B-20
7	19.6	12.0	70	3	US-09-364-540-21
8	19.4	11.8	43	3	US-09-991-181-34
9	19.4	11.8	43	3	US-09-990-444-34
10	19.4	11.8	43	3	US-09-997-333-34
11	19.4	11.8	43	3	US-09-992-598-34
12	19.4	11.8	69	2	US-08-169-813-2
13	19.2	11.7	33	3	US-09-000-630C-6
14	19.2	11.7	33	3	US-08-862-730C-6
15	19	11.6	69	3	US-09-270-767-30297
16	18.6	11.3	47	3	US-09-422-978-377
17	18.4	11.2	47	3	US-09-422-978-14
18	18.4	11.2	51	3	US-09-443-199C-329
19	18.4	11.2	74	3	US-09-513-999C-17717
20	18.2	11.1	40	2	US-08-425-684-88
21	18.2	11.1	40	2	US-08-675-502-88
22	18.2	11.1	40	3	US-09-245-802-88
23	18.2	11.1	50	3	US-10-131-827-5128
24	18.2	11.1	59	3	US-09-513-999C-14163

Sequence 3, Appli	US-09-142-722-3	18	11.0	25	18
Sequence 946, App	US-09-443-199C-946	51	11.0	26	18
Sequence 1, Appli	US-08-544-087A-1	66	11.0	27	18
Sequence 18, Appli	US-09-364-540-18	70	11.0	28	18
Sequence 19, Appli	US-08-753-247-19	72	11.0	29	18
Sequence 36, Appli	US-07-795-859B-36	45	10.9	30	17.8
Sequence 36, Appli	US-08-457-618-36	45	10.9	31	17.8
Sequence 244, App	US-08-171-389-244	50	10.9	32	17.8
Sequence 244, App	US-08-123-936-244	50	10.9	33	17.8
Sequence 244, App	US-08-475-228A-244	50	10.9	34	17.8
Sequence 244, App	US-08-482-080A-244	50	10.9	35	17.8
Sequence 244, App	US-09-354-947-244	50	10.9	36	17.8
Sequence 244, App	US-09-393-346-244	50	10.9	37	17.8
Sequence 244, App	PCT-US93-12388-244	50	10.9	38	17.8
Sequence 9, Appli	US-09-339-913B-9	60	10.9	39	17.8
Sequence 9, Appli	US-09-339-904A-9	60	10.9	40	17.8
Sequence 9, Appli	US-08-769-062B-9	60	10.9	41	17.8
Sequence 9, Appli	US-09-344-002B-9	60	10.9	42	17.8
Sequence 9, Appli	US-09-559-565C-9	60	10.9	43	17.8
Sequence 9, Appli	US-09-693-350-9	60	10.9	44	17.8
Sequence 9, Appli	US-09-693-389-9	60	10.9	45	17.8
Sequence 9, Appli	US-09-559-671A-9	60	10.9	46	17.8
Sequence 9, Appli	US-09-339-926A-9	60	10.9	47	17.8
Sequence 9, Appli	US-09-954-692-9	60	10.9	48	17.8
Sequence 32, Appli	US-10-903-350-32	64	10.9	49	17.8
Sequence 33, Appli	US-10-903-350-33	64	10.9	50	17.8
Sequence 29198, A	US-09-513-999C-29198	74	10.9	51	17.8
Sequence 18, Appli	US-09-320-424-18	77	10.9	52	17.8
Sequence 18, Appli	US-09-825-563-18	77	10.9	53	17.8
Sequence 33, Appli	US-08-253-155A-93	44	10.7	54	17.6
Sequence 22, Appli	US-08-625-209A-22	44	10.7	55	17.6
Sequence 22, Appli	US-08-853-733B-22	44	10.7	56	17.6
Sequence 1176, Ap	US-09-443-199C-1176	51	10.7	57	17.6
Sequence 28, Appli	US-08-151-574-28	56	10.7	58	17.6
Sequence 28, Appli	US-08-419-448-28	56	10.7	59	17.6
Sequence 28, Appli	US-09-233-510-28	56	10.7	60	17.6
Sequence 7, Appli	US-08-836-561-7	58	10.7	61	17.6
Sequence 8, Appli	US-08-836-561-8	64	10.7	62	17.6
Sequence 1, Appli	US-09-434-123-8	64	10.7	63	17.6
Sequence 1, Appli	US-09-050-516-1	67	10.7	64	17.6
Sequence 49, Appli	US-10-278-547-1	67	10.7	65	17.6
Sequence 444, App	US-09-422-978-444	30	10.6	66	17.4
Sequence 608, App	US-09-443-199C-608	51	10.6	67	17.4
Sequence 6, Appli	US-09-621-625A-6	57	10.6	68	17.4
Sequence 113025,	US-09-396-196G-113025	25	10.5	69	17.4
Sequence 135, App	US-09-422-978-135	47	10.5	70	17.4
Sequence 1827, Ap	US-10-131-827-1827	50	10.5	71	17.2
Patent No. 5258287	5258287-20	61	10.5	72	17.2
Sequence 7, Appli	US-09-463-458A-7	72	10.5	73	17.2
Sequence 9028, Ap	US-09-396-196G-9028	25	10.4	74	17.2
Sequence 15810, A	US-09-396-196G-15810	25	10.4	75	17.2
Sequence 100928,	US-09-396-196G-100928	25	10.4	76	17.2
Sequence 100930,	US-09-396-196G-100930	25	10.4	77	17.2
Sequence 6988, Ap	US-08-584-040-6988	27	10.4	78	17.2
Sequence 974, App	US-09-671-317-974	47	10.4	79	17.2
Sequence 180, App	US-09-422-978-180	47	10.4	80	17.2
Sequence 1448, Ap	US-09-422-978-1448	47	10.4	81	17.2
Sequence 1878, Ap	US-09-422-978-1878	47	10.4	82	17.2
Sequence 486, App	US-10-131-827-486	50	10.4	83	17.2
Sequence 21, Appli	US-08-477-270-21	62	10.4	84	17.2
Sequence 48, Appli	US-09-586-546-48	66	10.4	85	17.2
Sequence 9, Appli	US-09-065-914B-9	66	10.4	86	17.2
Sequence 27734, A	US-09-513-999C-27734	71	10.4	87	17.2
Sequence 6996, Ap	US-09-270-767-6996	74	10.4	88	17.2
Sequence 22278, A	US-09-270-767-22278	74	10.4	89	17.2
Patent No. 5182195	5182195-3	77	10.4	90	17.2
Sequence 7348, Ap	US-09-396-196G-7348	25	10.2	91	17.2
Sequence 11869, A	US-09-371-772B-11869	38	10.2	92	17.2
Sequence 591, App	US-09-671-317-591	96	10.2	93	17.2
Sequence 1071, Ap	US-09-422-978-1071	47	10.2	94	16.8
				95	16.8
				96	16.8
				97	16.8





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/ HYPOTHETICAL: no
/ ANTI-SENSE:
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: bromo mosaic virus
/ STRAIN: Madison
/ INDIVIDUAL ISOLATE: M1
/ DEVELOPMENTAL STAGE:
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE:
/ CELL LINE:
/ ORGANELLE:
/ IMMEDIATE SOURCE:
/ LIBRARY: no
/ CLONE:
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION: BMV RNA1
/ UNITS:
/ FEATURE:
/ NAME/KEY: lower strand capable of forming a heteroduplex with SEQ ID 3 (het
/ NAME/KEY: in Fig. 3)
/ LOCATION:
/ IDENTIFICATION METHOD: cDNA sequencing
/ OTHER INFORMATION:
/ PUBLICATION INFORMATION:
/ AUTHORS: Nagy, P.D.
/ AUTHORS: Bujarski, J.J.
/ TITLE: Targeting the site of RNA-RNA recombination in virus with antisense
/ JOURNAL: Proc. Natl. Acad. Sci. USA
/ VOLUME: 90
/ ISSUE:
/ PAGES: 6390-6394
/ DATE: July 1993
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE: July 1993
/ RELEVANT RESIDUES IN SEQ ID NO: 66
/
US-08-089-974B-4
Query Match 12.3%; Score 20.2; DB 2; Length 78;
Best Local Similarity 56.9%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 87 CTTACCCGGGAGGAGTGCGAGCGAGTGCACAGACACAGCGCATCCTTAAACATCTGAGCTC 146
Ddb 75 CTCCTCTCAGCAGAGGTCTCACAGACACAGCGCATCCTTAAACATCTGAGCTC 16
QY 147 AAATC 151
Ddb 15 AAATC 11
RESULT 5
US-08-089-974B-18/c
; Sequence 18, Application US/08089974B
; Patent No. 5877401
; GENERAL INFORMATION:
; APPLICANT: Bujarski, Jozef J.
; APPLICANT: Nagy, Peter D.
; TITLE OF INVENTION: Targeting and Enhancing RNA-RNA Recombination
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Grace J. Fishel
; STREET: 929 Fee Fee, Suite 100
; CITY: St. Louis, MO
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 300 KB storage
; COMPUTER: Hewlett Packard Vectra

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LOCATION: BMV RNAL/BMV RNA3  
IDENTIFICATION METHOD: cDNA sequencing  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS: Nagy, P.D.  
AUTHORS: Bujarski, J.J.  
TITLE: Targeting the site of RNA-RNA recombination in virus with antisense s  
JOURNAL: Proc. Natl. Acad. Sci. USA  
VOLUME: 90  
ISSUE:  
PAGES: 6390-6394  
DATE: July 1993  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE: July 1993  
RELEVANT RESIDUES IN SEQ ID NO: 67

US-08-089-974B-20

Query Match 12.3%; Score 20.2; DB 2; Length 78;

Best Local Similarity 56.9%; Pred. No. 1.4e+03;

Matches 37; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 87 CTTACCCCGGAGGAGGTCAGCCAGCTGCAAGCCCAAGTGAAGAACATCTGAGCTC 146

Db 75 CTCCTCAGAGGAGGTCCTCACAGACAGAGCGCATCATCTTACACAAATTAAGATC 16

QY 147 AAATC 151

Db 15 AAATC 11

#### RESULT 7

US-09-364-540-21/c

Sequence 21, Application US/09364540A

Patent No. 6762290

GENERAL INFORMATION:

APPLICANT: Janjic, Nebojsa

APPLICANT: Gold, Larry

TITLE OF INVENTION: High Affinity Vascular Endothelial Growth Factor (VEGF)

TITLE OF INVENTION: Receptor Nucleic Acid Ligands and Inhibitors

FILE REFERENCE: NEX88

CURRENT APPLICATION NUMBER: US/09/364,540A

CURRENT FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 21

LENGTH: 70

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: modified base

LOCATION: (1)..(70)

OTHER INFORMATION: All pyrimidines are 2'F.

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

US-09-364-540-21

Query Match

Best Local Similarity 12.0%; Score 19.6; DB 3; Length 70;

Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 18 GAGGGAGCTGGCGAGTCTTAGACAGTCCGGAAGTTCTCAAGGCACAGGTC 67

Db 64 GAGTGTCTGACAGGAGCAGCAAAATACGAAGTTCCAAAGGACGACCTC 15

#### RESULT 8

US-09-991-181-34

Sequence 34, Application US/09991181

Patent No. 6913919

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austen L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P2730PICS3  
CURRENT APPLICATION NUMBER: US/09/991,181  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 11.8%; Score 19.4; DB 3; Length 43;  
Best Local Similarity 70.3%; Pred. No. 2e+03;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 79 TGACTGCTCTTACCCGGGAGGACGTGGAGCCAGCT 115  
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Db 1 TGACTGCTCTTACCCGGGAGGACGTGGAGCCAGCT 37  
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RESULT 9  
US-09-990-444-34  
; Sequence 34, Application US/09990444  
; Patent No. 6930170  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C19  
CURRENT APPLICATION NUMBER: US/09/990,444  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472





APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-16  
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PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690



Query Match 11.8%; Score 19.4; DB 3; Length 43;  
Best Local Similarity 70.3%; Pred. No. 2e+03;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 79 TGACTGCTCTTACCCCGGAGCAGTCGAGCCAGCT 115  
DB 1 TGACTGCACTACCCCGTGGCAAGCTGTGAGCCAGCT 37

RESULT 12  
US-08-169-813-2  
Sequence 2, Application US/08169813  
Patent No. 5591823  
GENERAL INFORMATION:  
APPLICANT: Hung, Paul P.  
APPLICANT: Lee, Shaw-Guang L.  
APPLICANT: Kalyan, Narendra K.  
TITLE OF INVENTION: EXPRESSION OF SPECIFIC IMMUNOGENS  
TITLE OF INVENTION: USING VIRAL ANTIGENS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby, P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5, inch, 360 kb storage  
COMPUTER: Emerson 16MHz  
OPERATING SYSTEM: DOS 3.3  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,813  
FILING DATE: 17-DEC-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: 07/805,105  
FILING DATE: 11-Dec-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Robert Schaffer, Esq.  
REGISTRATION NUMBER: 31,194  
REFERENCE/DOCKET NUMBER: 0632/06916

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 527-7700  
TELEFAX: (212) 753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: unknown  
FEATURE:  
OTHER INFORMATION: Anti-sense strand begins four  
bases before the sense strand,  
OTHER INFORMATION: adding the sequence CCGG and  
OTHER INFORMATION: ends four bases before the  
sense strand.

US-08-169-813-2

Query Match 11.8%; Score 19.4; DB 2; Length 69;  
Best Local Similarity 60.4%; Pred. No. 2.5e+03;  
Matches 32; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 30 CAGTTCTACAGAGTCCCGAAGTTCTCAAGGCACAGCTCTCTTCTGAC 82  
DB 3 CAGTACTACAGAGCCCGCAAAACCAAGGATCAGGATTCCTTTGATTCAC 55

RESULT 13  
US-09-000-630C-6  
Sequence 6, Application US/09000630C  
Patent No. 6018029  
GENERAL INFORMATION:  
APPLICANT: Fuller, Gerald M.  
APPLICANT: Fuentes, Nelson L.  
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor  
TITLE OF INVENTION: Antagonist  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White  
STREET: 2001 Park Place, Suite 1400  
CITY: Birmingham  
STATE: Alabama  
COUNTRY: USA  
ZIP: 35203-2736  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch,  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Microsoft Windows  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/000,630C  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,730  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide

Query Match 11.7%; Score 19.2; DB 3; Length 33;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCGGGGAGCAGTCGAGCCAGCTGCAAGCC 122  
DB 2 CCTCTGGGAGAAATCCAGCAAGATGCAAGCC 33

```

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 377
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-14615-65 : polymorphic base A or G
US-09-422-978-377

Query Match 11.3%; Score 18.6; DB 3; Length 47;
Best Local Similarity 62.8%; Pred. No. 4.1e+03;
Matches 27; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

QY 26 TGGCAGGTTCTAGACAGTCCGGAAGTTCTCAAGGCACAGTCT 68
Db 2 TGGCAATTTTTTTAGAGTCCCGTGGTAAAGGCACTGTCT 44

RESULT 17
US-09-422-978-14
; Sequence 14, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.2%; Score 18.4; DB 3; Length 47;
Best Local Similarity 69.4%; Pred. No. 4.9e+03;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 68 TCTTCTCGTTTGTGCTGCTTACCCCGGGAGGCA 103
Db 2 TCTCCCTGGTAAGTCGGTTCTTTCAGGGAAGCA 37

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.6%; Score 19; DB 3; Length 69;
Best Local Similarity 60.8%; Pred. No. 3.5e+03;
Matches 31; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 20 GGGAGCTGGCGAGTTCTAGACAGTCCGGAAGTTCTCAAGGCACAGTCTCT 70
Db 60 GGCAGCGGGGAAGTTTCATCGTAAACGGGAAGATCACATATGGCGAGGCTCT 10

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.7%; Score 19.2; DB 3; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCAGGAGGAGTGCAGCAGTGCAGGCGCAAGCC 122
Db 2 CCTCTGGGAGAAATCCAGCAGATGCAGGCGCAAGCC 33

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.7%; Score 19.2; DB 3; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCAGGAGGAGTGCAGCAGTGCAGGCGCAAGCC 122
Db 2 CCTCTGGGAGAAATCCAGCAGATGCAGGCGCAAGCC 33

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.7%; Score 19.2; DB 3; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCAGGAGGAGTGCAGCAGTGCAGGCGCAAGCC 122
Db 2 CCTCTGGGAGAAATCCAGCAGATGCAGGCGCAAGCC 33

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.7%; Score 19.2; DB 3; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCAGGAGGAGTGCAGCAGTGCAGGCGCAAGCC 122
Db 2 CCTCTGGGAGAAATCCAGCAGATGCAGGCGCAAGCC 33

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 14
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-12503-44 : polymorphic base G or C
US-09-422-978-14

Query Match 11.7%; Score 19.2; DB 3; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCAGGAGGAGTGCAGCAGTGCAGGCGCAAGCC 122
Db 2 CCTCTGGGAGAAATCCAGCAGATGCAGGCGCAAGCC 33

; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 117
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Query Match	11.28	Score 18.4	DB 3	Length 51
Best Local Similarity	69.44	Pred.No. 5.1e+03		
Matches	25	Conservative 0	Mismatches 11	Indels 0
Gaps	0			

```

US-09-513-999C-17717
; Sequence 17717, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 17717
; LENGTH: 74
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-17717

```

Oy	120	GCCCCACA	127
Dδ	67	GCCCCACA	74

RESULT 20  
US-08-425-684-88  
; Sequence 88, Application US/08425684  
; Patent No. 5834252  
; GENERAL INFORMATION:  
; APPLICANT: STEMMER PH.D., WILLEM P.C.  
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW  
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,684  
; FILING DATE: 18-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIUNN ESO., TRACY J.  
; REGISTRATION NUMBER: 34,587  
; REFERENCE/DOCKET NUMBER: 16528U-015400US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; US-08-425-684-88

Query Match 11.1%; Score 18.2; DB 2; Length 40;  
Best Local Similarity 74.2%; Pred. No. 5.4e+03;  
Matches 23; Conservative 0; Mismatches 8; Indels

**Qy**      124 CACAGTGAAGAACAATCTGAGCTCAAAATCCAG 154  
          | | | | | | | | | | | | | | | |  
**Db**      10 CGCAGGAAGAACAATGTGAGCAAAGGCCAG 40

RESULT 21

```

RES001 21
US-08-675-502-88
; Sequence 88, Application US/08675502
; Patent No. 5928905
;
; GENERAL INFORMATION:
;
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,502
; FILING DATE: 03-JUL-1996

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```

; INFORMATION FOR SEQ ID NO: 88:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 40 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: circular
;
US-09-245-802-88

Query Match          11.1%; Score 18.2; DB 3; Length 40;
Best Local Similarity 74.2%; Pred. No. 5.4e+03;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 124 CACAGTGAAGACATCTGAGCTCAAAATCCAG 154
      ||| ||||| ||||| || ||||
Db 10 CGCAGGAAGACATGTGAGCAAAAGGCCAG 40

RESULT 23
US-10-131-827-5128
; Sequence 5128, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING A
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5128
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5128

Query Match          11.1%; Score 18.2; DB 3; Length 50;
Best Local Similarity 66.7%; Pred. No. 6e+03;
Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 99 AGCAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGAACA 137
      ||||| ||| ||| ||| ||| ||| |||
Db 4 AGGCAGACGAGAGAGCGGAGGTCTCAGAGTGAACCACA 42

RESULT 24
US-09-513-999C-14163/c
; Sequence 14163, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14163
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Homo sapiens

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Job time : 216.424 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds  
(without alignments)  
673.188 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18

Sequence: 1 tgccttgagaacttcggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	9	US-10-182-049-21
C 2	14.8	82.2	25	10	US-11-036-317-592184
C 3	14.8	82.2	25	10	US-11-036-317-812924
C 4	14.8	82.2	25	10	US-11-060-756-162369
C 5	14.4	80.0	25	7	US-10-719-956-352445
C 6	14.4	80.0	25	10	US-11-036-317-142883
C 7	14	77.8	25	8	US-10-719-900-511931
C 8	14	77.8	25	8	US-10-719-900-581095
C 9	13.8	76.7	20	7	US-10-380-126-36
C 10	13.8	76.7	20	5	US-10-098-263B-93346
C 11	13.8	76.7	25	7	US-10-719-956-524451
C 12	13.8	76.7	25	7	US-10-719-956-684475
C 13	13.8	76.7	25	10	US-11-036-317-43312
C 14	13.8	76.7	25	10	US-11-036-317-65279
C 15	13.4	74.4	25	7	US-10-719-956-207934
C 16	13.4	74.4	25	7	US-10-719-956-254482
C 17	13.4	74.4	25	7	US-10-719-956-306955
C 18	13.4	74.4	25	7	US-10-719-956-418803
C 19	13.4	74.4	25	7	US-10-719-956-429526
C 20	13.4	74.4	25	7	US-10-719-956-442037
C 21	13.4	74.4	25	8	US-10-719-900-346702
C 22	13.4	74.4	25	8	US-10-719-900-833460
C 23	13.4	74.4	25	8	US-10-719-900-878385

Sequence 440654,	25	10	US-11-036-317-440654	74.4	C 24
Sequence 701048,	25	10	US-11-036-317-701048	74.4	C 25
Sequence 748820,	25	10	US-11-036-317-748820	74.4	C 26
Sequence 282, App	25	6	US-10-722-939-282	73.4	C 27
Sequence 8979, Ap	21	6	US-10-131-827-8979	73.4	C 28
Sequence 2, Appl	25	3	US-09-727-0300-2	73.3	C 29
Sequence 45113, A	25	7	US-10-719-956-45113	73.3	C 30
Sequence 244426,	25	7	US-10-719-956-244426	73.3	C 31
Sequence 280310,	25	7	US-10-719-956-280310	73.3	C 32
Sequence 198900,	25	7	US-10-719-956-198900	73.3	C 33
Sequence 406389,	25	7	US-10-719-956-406389	73.3	C 34
Sequence 468942,	25	7	US-10-719-956-468942	73.3	C 35
Sequence 659705,	25	7	US-10-719-956-659705	73.3	C 36
Sequence 43968,	25	8	US-10-719-900-434968	73.3	C 37
Sequence 521447,	25	8	US-10-719-900-521447	73.3	C 38
Sequence 959400,	25	8	US-10-719-900-959400	73.3	C 39
Sequence 962421,	25	8	US-10-719-900-962421	73.3	C 40
Sequence 978806,	25	8	US-10-719-900-978806	73.3	C 41
Sequence 1069, Ap	25	9	US-10-809-189-1069	73.3	C 42
Sequence 54888, A	25	9	US-10-809-189-54888	73.3	C 43
Sequence 68119, A	25	9	US-10-809-189-68119	73.3	C 44
Sequence 106398,	25	10	US-11-036-317-106398	73.3	C 45
Sequence 434343,	25	10	US-11-036-317-434343	73.3	C 46
Sequence 592185,	25	10	US-11-036-317-592185	73.3	C 47
Sequence 692836,	25	10	US-11-036-317-692836	73.3	C 48
Sequence 702596,	25	10	US-11-036-317-702596	73.3	C 49
Sequence 812925,	25	10	US-11-036-317-812925	73.3	C 50
Sequence 30, Appl	60	9	US-10-491-192-30	73.3	C 51
Sequence 25193, A	65	3	US-09-908-975-25193	73.3	C 52
Sequence 8222, Ap	25	7	US-10-719-956-8222	72.2	C 53
Sequence 180832,	25	7	US-10-719-956-180832	72.2	C 54
Sequence 574078,	25	7	US-10-719-956-574078	72.2	C 55
Sequence 634205,	25	7	US-10-719-956-634205	72.2	C 56
Sequence 242896,	25	8	US-10-719-900-242896	72.2	C 57
Sequence 550865,	25	8	US-10-719-900-550865	72.2	C 58
Sequence 39222, A	25	10	US-11-036-317-39222	72.2	C 59
Sequence 439994,	25	10	US-11-036-317-439994	72.2	C 60
Sequence 446604,	25	10	US-11-036-317-446604	72.2	C 61
Sequence 719852,	25	10	US-11-036-317-719852	72.2	C 62
Sequence 733366,	25	10	US-11-036-317-733366	72.2	C 63
Sequence 893293,	25	10	US-11-036-317-893293	72.2	C 64
Sequence 902015,	25	10	US-11-036-317-902015	72.2	C 65
Sequence 24456, A	65	3	US-09-908-975-24456	72.2	C 66
Sequence 3717, Ap	24	3	US-09-940-185-3717	71.1	C 67
Sequence 59369, A	25	7	US-10-681-773-59369	71.1	C 68
Sequence 6043, Ap	25	7	US-10-719-956-6043	71.1	C 69
Sequence 15596, A	25	7	US-10-719-956-15596	71.1	C 70
Sequence 138463,	25	7	US-10-719-956-138463	71.1	C 71
Sequence 144685,	25	7	US-10-719-956-144685	71.1	C 72
Sequence 246078,	25	7	US-10-719-956-246078	71.1	C 73
Sequence 246079,	25	7	US-10-719-956-246079	71.1	C 74
Sequence 352444,	25	7	US-10-719-956-352444	71.1	C 75
Sequence 379329,	25	7	US-10-719-956-379329	71.1	C 76
Sequence 620584,	25	7	US-10-719-956-620584	71.1	C 77
Sequence 57032, A	25	8	US-10-719-900-57032	71.1	C 78
Sequence 498880,	25	8	US-10-719-900-498880	71.1	C 79
Sequence 967461,	25	8	US-10-719-900-967461	71.1	C 80
Sequence 107068,	25	10	US-11-036-317-107068	71.1	C 81
Sequence 235531,	25	10	US-11-036-317-235531	71.1	C 82
Sequence 235532,	25	10	US-11-036-317-235532	71.1	C 83
Sequence 251167,	25	10	US-11-036-317-251167	71.1	C 84
Sequence 419259,	25	10	US-11-036-317-419259	71.1	C 85
Sequence 434919,	25	10	US-11-036-317-434919	71.1	C 86
Sequence 462939,	25	10	US-11-036-317-462939	71.1	C 87
Sequence 861174,	25	10	US-11-036-317-861174	71.1	C 88
Sequence 153736,	25	10	US-11-060-756-153736	71.1	C 89
Sequence 153735,	25	10	US-11-060-756-153735	71.1	C 90
Sequence 182816,	25	10	US-11-060-756-182816	71.1	C 91
Sequence 182817,	25	10	US-11-060-756-182817	71.1	C 92
Sequence 196898,	25	10	US-11-060-756-196898	71.1	C 93
Sequence 196899,	25	10	US-11-060-756-196899	71.1	C 94
Sequence 30, Appl	20	10	US-11-122-741-30	68.9	C 95

97 12.4 68.9 21 8 US-10-751-736-53330 Sequence 53330, A  
98 12.4 68.9 22 3 US-09-998-547-5 Sequence 5, Appli  
99 12.4 68.9 22 8 US-10-819-714-5 Sequence 5, Appli  
100 12.4 68.9 25 7 US-10-717-597-2349 Sequence 2349, Ap

## ALIGNMENTS

RESULT 1  
US-10-182-049-21  
; Sequence 21, Application US/10182049  
; Publication No. US2005011322A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION  
; FILE REFERENCE: RTSP-0360  
; CURRENT APPLICATION NUMBER: US/10/182,049  
; CURRENT FILING DATE: 2002-07-27  
; PRIOR APPLICATION NUMBER: 09/490,208  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 182  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-182-049-21

Query Match 100.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TGCCTTGAGAACTTCGGG 18  
Db 1 TGCCTTGAGAACTTCGGG 18  
|||||  
|||||

RESULT 2  
US-11-036-317-592184/c  
; Sequence 592184, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 592184  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-592184

Query Match 82.2%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 4.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TGCCTTGAGAACTTCGGG 18  
Db 19 TGCCTTGAGGAATTCGGG 2  
|||||  
|||||

RESULT 3

US-11-036-317-812924  
; Sequence 812924, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 812924  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-812924

Query Match 82.2%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 4.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TGCCTTGAGAACTTCGGG 18  
Db 6 TGCCTTGAGAACTTCGGG 23  
|||||  
|||||

RESULT 4  
US-11-060-756-162369/c  
; Sequence 162369, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 162369  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-162369

Query Match 82.2%; Score 14.8; DB 10; Length 25;  
Best Local Similarity 88.9%; Pred. No. 4.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 TGCCTTGAGAACTTCGGG 18  
Db 24 TGCCTTAAAGAACTTAGGG 7  
|||||  
|||||

RESULT 5  
US-10-719-956-352445/c  
; Sequence 352445, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 352445



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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-352445

Query Match      80.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 8e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 3 CCTTGAGAACTTCGGG 18
   |||||
Db 22 CCTTGAGACCTTCGGG 7

RESULT 6
US-11-036-317-142883/c
; Sequence 142883, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 142883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-142883

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 8e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 3 CCTTGAGAACTTCGGG 18
   |||||
Db 25 CCTTGAGAACTTCGGG 10

RESULT 7
US-10-719-900-511931
; Sequence 511931, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse.
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 511931
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-511931

Query Match      77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14
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Db 9 TGCCTTGAGAACTT 22

US-10-655-801-21.max.rnpbm
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RESULT 8
US-10-719-900-581095/c
; Sequence 581095, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 581095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-581095

Query Match      77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTCGG 17
   |||||
Db 24 CTTGAGAACTTCGG 11

RESULT 9
US-10-380-126-36/c
; Sequence 36, Application US/10380126
; Publication No. US20040029824A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTSP-0175
; CURRENT APPLICATION NUMBER: US/10/380,126
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/657,042
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-126-36

Query Match      76.7%; Score 13.8; DB 7; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18
   |||||
Db 18 GCCTTGAGAACTTCAGG 2

RESULT 10
US-10-098-263B-93346/c
; Sequence 93346, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
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; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 93346  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-93346

Query Match 76.7%; Score 13.8; DB 5; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCTTGAGAACTTCGG 17  
||||| ||||| |||||  
Db 23 TGCCTTAAGAAGCTCGG 7

RESULT 11  
US-10-719-956-542451/c  
; Sequence 542451, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; PRIOR FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 542451  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-542451

Query Match 76.7%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18  
||||| ||||| |||||  
Db 22 GCCTTGAGAACTTCGG 6

RESULT 12  
US-10-719-956-684475/c  
; Sequence 684475, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; PRIOR FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 684475  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-684475

Query Match 76.7%; Score 13.8; DB 7; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCTTGAGAACTTCGG 17  
||||| ||||| |||||  
Db 21 TGCCTTAAGAAGCTTCGG 5

RESULT 13  
US-11-036-317-43312  
; Sequence 43312, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 43312  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-43312

Query Match 76.7%; Score 13.8; DB 10; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18  
||||| ||||| |||||  
Db 2 GCCATGAGAACTTCGAG 18

RESULT 14  
US-11-036-317-65279  
; Sequence 65279, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 65279  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-65279

Query Match 76.7%; Score 13.8; DB 10; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18  
||||| ||||| |||||  
Db 8 GCCATGAGAACTTCGAG 24

RESULT 15  
US-10-719-956-207934  
; Sequence 207934, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 207934  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-207934

Query Match 74.4%; Score 13.4; DB 7; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15  
 Db 2 TTCCCTTGAGAACTTC 16

RESULT 16  
 US-10-719-956-254482  
 ; Sequence 254482, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; PRIOR FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 254482  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-254482

Query Match 74.4%; Score 13.4; DB 7; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCGG 17  
 Db 1 CCTTGAGAACTTCGG 15

RESULT 17  
 US-10-719-956-306955/c  
 ; Sequence 306955, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; PRIOR FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 306955  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-306955

Query Match 74.4%; Score 13.4; DB 7; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15

Db 15 TGCAATTGAGAACTTC 1

RESULT 18  
 US-10-719-956-418803/c  
 ; Sequence 418803, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 418803  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-418803

Query Match 74.4%; Score 13.4; DB 7; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15  
 Db 16 TGCCCTTGAGAACTTC 2

RESULT 19  
 US-10-719-956-429526/c  
 ; Sequence 429526, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 429526  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-429526

Query Match 74.4%; Score 13.4; DB 7; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15  
 Db 16 TGCCCTTGAGAACTTC 2

RESULT 20  
 US-10-719-956-442037  
 ; Sequence 442037, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 442037  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-442037

Query Match 74.4%; Score 13.4; DB 7; Length 25;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GCCTTGAGAACTTCG 16  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 GCCTTGAGAACTTAG 16

RESULT 21  
US-10-719-900-346702/c  
; Sequence 346702, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 346702  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-346702

Query Match 74.4%; Score 13.4; DB 8; Length 25;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CTTGAGAACTTCGG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 15 CTTGAGAACTTCGG 1

RESULT 22  
US-10-719-900-833460  
; Sequence 833460, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 833460  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-833460

Query Match 74.4%; Score 13.4; DB 8; Length 25;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TGCCTTGAGAACTTC 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 TGCCTTGAGAACTTC 17

RESULT 23  
US-10-719-900-878385/c  
; Sequence 878385, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 878385  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-878385

Query Match 74.4%; Score 13.4; DB 8; Length 25;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TGCCTTGAGAACTTC 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 17 TGCCTTGAGAACTTC 3

RESULT 24  
US-11-036-317-440654/c  
; Sequence 440654, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 440654  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-440654

Query Match 74.4%; Score 13.4; DB 10; Length 25;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CTTGAGAACTTCGG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 CTTGAGAACTTCGG 7

RESULT 25  
US-11-036-317-701048/c  
; Sequence 701048, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639

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; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 701048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-701048

Query Match      74.4%; Score 13.4; DB 10; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TGCCTTGAGAACTTC 15
        |||||
Db      25 TGCCTTGAGAGCTTC 11

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Job time : 223.11 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds  
(without alignments)  
403.294 Million cell updates/sec

**Title:** US-10-655-801-21

Perfect score: 18  
Sequence: 1 tgccttgagaacttcggg 18

Scoring table: IDENTITY\_NUC

**အိတ် ချည်ကပ် / အိတ် သီချည်ကပ်**

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

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Minimum DB seq length: 0
Maximum DB seq length: 80
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100

Database : Published Applications NA New: \*

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2: /cgn2_6/ptodata/1/pubpna/us06_new_pub.seq:
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8: /cgn2_6/ptodata/1/pubpna/us10_new_pub.seq:
9: /cgn2_6/ptodata/1/pubpna/us11_new_pub.seq:
10: /cgn2_6/ptodata/1/pubpna/us11_new_pub.seq:
11: /cgn2_6/ptodata/1/pubpna/us11_new_pub.seq:
12: /cgn2_6/ptodata/1/pubpna/us11_new_pub.seq:
13: /cgn2_6/ptodata/1/pubpna/us60_new_pub.seq:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	14	77.8	19	10	US-11-101-244-1087177		Sequence 1087177,
2	14	77.8	19	11	US-11-083-784-1087177		Sequence 1087177,
c 3	13.8	76.7	21	8	US-10-310-914A-249584		Sequence 249584,
4	13.8	76.7	25	12	US-11-121-849-233627		Sequence 233627,
5	13.8	76.7	25	12	US-11-121-849-310353		Sequence 310353,
6	13.8	76.7	61	8	US-10-310-914A-4446		Sequence 4446, Ap
7	13.8	76.7	63	8	US-10-310-914A-12044		Sequence 12044, A
8	13.8	76.7	78	8	US-10-310-914A-7665		Sequence 7665, Ap
c 9	13.4	74.4	19	10	US-11-101-244-644548		Sequence 644548,
10	13.4	74.4	19	10	US-11-101-244-1499872		Sequence 1499872,
c 11	13.4	74.4	19	11	US-11-101-244-1506108		Sequence 1506108,
c 12	13.4	74.4	19	11	US-11-083-784-644548		Sequence 644548,
c 13	13.4	74.4	19	11	US-11-083-784-1499872		Sequence 1499872,
c 14	13.4	74.4	19	11	US-11-083-784-1506108		Sequence 1506108,
c 15	13.4	74.4	30	8	US-10-857-780-3518		Sequence 3518, Ap
c 16	13.2	73.3	22	8	US-10-310-914A-1205266		Sequence 1205266,
c 17	13.2	73.3	24	8	US-10-310-914A-346426		Sequence 346426, A
c 18	13.2	73.3	25	12	US-11-121-849-27119		Sequence 27119, A
c 19	13.2	73.3	25	12	US-11-121-849-235259		Sequence 235259,
c 20	13.2	73.3	25	12	US-11-121-849-289504		Sequence 289504,

Sequence 471388,  
Sequence 471389,  
Sequence 471390,  
Sequence 608376,  
Sequence 50275, A  
Sequence 50276, A  
Sequence 50283, A

94 12.4 68.9 25 12 US-11-121-849-471388  
95 12.4 68.9 25 12 US-11-121-849-471389  
96 12.4 68.9 25 12 US-11-121-849-471390  
97 12.4 68.9 25 12 US-11-121-849-608376  
98 12.4 68.9 25 12 US-11-136-527-50275  
99 12.4 68.9 25 12 US-11-136-527-50276  
100 12.4 68.9 25 12 US-11-136-527-50283

## ALIGNMENTS

## RESULT 1

US-11-101-244-1087177  
; Sequence 1087177, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1087177  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1087177

Query Match 77.8%; Score 14; DB 10; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15  
Db 1 GCCUUGAGAACUUC 14  
||||:|||||

## RESULT 2

US-11-083-784-1087177  
; Sequence 1087177, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1087177  
; LENGTH: 19

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1087177

Query Match 77.8%; Score 14; DB 11; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15  
Db 1 GCCUUGAGAACUUC 14  
||||:|||||

## RESULT 3

US-10-310-914A-249584/c  
; Sequence 249584, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 249584  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-249584

Query Match 76.7%; Score 13.8; DB 8; Length 21;  
Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGG 17  
Db 17 TGCCTTGAGAAATTCG 1  
|||||

## RESULT 4

US-11-121-849-233627  
; Sequence 233627, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 233627  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-233627

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18  
Db 3 GCCTTGAGAACTTCGG 19  
|||||

## RESULT 5



```

US-11-121-849-310353
; Sequence 310353, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 310353
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-310353
Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGGG 18
Db 1 GCTTTGAGAACATCGGG 17
|||||
|

RESULT 6
US-10-310-914A-4446
; Sequence 4446, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4446
; LENGTH: 61
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-4446
Query Match 76.7%; Score 13.8; DB 8; Length 61;
Best Local Similarity 70.6%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGGG 18
Db 2 GCCUGGACAAACUUCGGG 18
|||||
|

RESULT 7
US-10-310-914A-12044/c
; Sequence 12044, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12044

```

QY 3 CCTTGAGAACTTCG 17  
|||||  
Db 15 CCTTGAGCACTTCG 1

## RESULT 10

US-11-101-244-1499872/c  
; Sequence 1499872, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1499872  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1499872

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 93.3%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTC 15  
|||||  
Db 17 TGCCTTGAGAGCTTC 3

## RESULT 11

US-11-101-244-1506108/c  
; Sequence 1506108, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1506108  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1506108

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 93.3%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCG 17  
|||||  
Db 18 CCTTAAGAACTTCG 4

## RESULT 12

US-11-083-784-644548/c  
; Sequence 644548, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 644548  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-644548

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
Best Local Similarity 93.3%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCG 17  
|||||  
Db 15 CCTTGAGCACTTCG 1

## RESULT 13

US-11-083-784-1499872/c  
; Sequence 1499872, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1499872  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1499872

Query Match 74.4%; Score 13.4; DB 11; Length 19;

```

Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15
    |||||
Db 17 TGCCCTTGAGAGCTTC 3

RESULT 14
US-11-083-784-1506108/c
; Sequence 1506108, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1506108
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1506108

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCGG 17
    |||||
Db 18 CCTTAAGAACTTCGG 4

RESULT 15
US-10-857-780-3518
; Sequence 3518, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAWMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RIKARD, RICHARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3518
; LENGTH: 30
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-857-780-3518

Query Match 74.4%; Score 13.4; DB 8; Length 30;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15
    |||||
Db 9 TGCCCTTGAGAACTTC 23

RESULT 16
US-10-310-914A-1205266/c
; Sequence 1205266, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1205266
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1205266

Query Match 73.3%; Score 13.2; DB 8; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTCGG 18
    |||||
Db 21 TGCCCTTGAGAACTTCAGG 4

RESULT 17
US-10-310-914A-346426/c
; Sequence 346426, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 346426
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-346426

Query Match 73.3%; Score 13.2; DB 8; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTCGG 18
    |||||
Db 21 TGCCCTTGAGAGCTCCGTG 4

RESULT 18

```

```
US-11-121-849-27119
; Sequence 27119, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27119
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-27119
Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
| | | | | | | | | | | | | | | | | | | | |
Db 4 TCCCGTGAGAACTTCTGG 21
| | | | | | | | | | | | | | | | | | | | |

RESULT 19
US-11-121-849-235259
; Sequence 235259, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 235259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235259
Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
| | | | | | | | | | | | | | | | | | | | |
Db 4 TCCCGTGAGAACTTCTGG 21
| | | | | | | | | | | | | | | | | | | | |

RESULT 19
US-11-121-849-235259
; Sequence 235259, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 235259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235259
Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
| | | | | | | | | | | | | | | | | | | | |
Db 4 TCCCGTGAGAACTTCTGG 21
| | | | | | | | | | | | | | | | | | | | |

RESULT 20
US-11-121-849-289504/c
; Sequence 289504, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 289504
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-289504
Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
| | | | | | | | | | | | | | | | | | | | |
Db 23 TGCCTTGAGAACTTCGGG 6
| | | | | | | | | | | | | | | | | | | | |

RESULT 21
US-11-121-849-346138
; Sequence 346138, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 346138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-346138
Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
| | | | | | | | | | | | | | | | | | | | |
Db 8 TGCCTTGAGAACTTCTGG 25
| | | | | | | | | | | | | | | | | | | | |

RESULT 22
US-11-121-849-448511/c
; Sequence 448511, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-448511
Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
| | | | | | | | | | | | | | | | | | | | |
```

Db 19 TGCCTTGAGGAACCTCGG 2

RESULT 23

US-11-121-849-448519/c  
 ; Sequence 448519, Application US/11121849  
 ; Publication No. US20050272080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
 ; TITLE OF INVENTION: Microarrays  
 ; FILE REFERENCE: 3684.1  
 ; CURRENT APPLICATION NUMBER: US/11/121,849  
 ; CURRENT FILING DATE: 2005-05-03  
 ; PRIOR APPLICATION NUMBER: 60/567,949  
 ; PRIOR FILING DATE: 2004-05-03  
 ; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 448519  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-448519

Query Match 73.3%; Score 13.2; DB 12; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGGAACCTCGG 18

Db 23 TGCCTTGAGGAACCTCGG 6

RESULT 24

US-11-121-849-448520/c  
 ; Sequence 448520, Application US/11121849  
 ; Publication No. US20050272080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
 ; TITLE OF INVENTION: Microarrays  
 ; FILE REFERENCE: 3684.1  
 ; CURRENT APPLICATION NUMBER: US/11/121,849  
 ; CURRENT FILING DATE: 2005-05-03  
 ; PRIOR APPLICATION NUMBER: 60/567,949  
 ; PRIOR FILING DATE: 2004-05-03  
 ; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 448520  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-448520

Query Match 73.3%; Score 13.2; DB 12; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGGAACCTCGG 18

Db 21 TGCCTTGAGGAACCTCGG 4

RESULT 25

US-11-121-849-448521/c  
 ; Sequence 448521, Application US/11121849  
 ; Publication No. US20050272080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
 ; TITLE OF INVENTION: Microarrays  
 ; FILE REFERENCE: 3684.1  
 ; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03  
 ; PRIOR APPLICATION NUMBER: 60/567,949  
 ; PRIOR FILING DATE: 2004-05-03  
 ; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 448521  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-448521

Query Match 73.3%; Score 13.2; DB 12; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGGAACCTCGG 18

Db 19 TGCCTTGAGGAACCTCGG 2

Search completed: March 3, 2006, 07:56:43  
 Job time : 98.0559 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 8972.05 Seconds  
(without alignments)  
855.220 Million cell updates/sec

Title: us-10-655-801-3\_COPY\_14\_177  
Perfect score: 164  
Sequence: 1 tctcgccaccttgatgag.....tcaaatccagataagtaca 164

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hc:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	23.2	14.1	50	7	CF981901 maj75a12
C 2	23.2	14.1	58	10	CL639648
C 3	21.6	13.2	71	9	AZ791987 2M0043G08
C 4	21.2	12.9	72	7	CV305418 t162a05.b
C 5	21.2	12.9	72	7	CV305419 t162a05.g
C 6	20.8	12.7	66	3	BJ083039
C 7	20.8	12.7	75	8	H84929
C 8	20.6	12.6	67	9	AZ768319
C 9	20.6	12.6	74	10	CL603643
C 10	20.6	12.6	80	11	DQ051485
C 11	20.4	12.4	60	9	AZ829920
C 12	20.4	12.4	79	1	AA917946
C 13	20.2	12.3	57	10	CG869849
C 14	20.2	12.3	77	10	CL640815
C 15	20.2	12.3	77	4	AK198748
C 16	20.2	12.3	72	2	EG237470
C 17	19.8	12.1	64	9	AF149527
C 18	19.8	12.1	77	9	AZ615721
C 19	19.8	12.1	80	10	AG829487
C 20	19.8	12.1	80	10	CL869085
C 21	19.6	12.0	47	9	BH806710
C 22	19.6	12.0	74	10	CG712884

AG217126 Drosophila	78	10	AG217126
AL462137 T. brucei	59	11	TA112C05Q
CG638372 OST367812	62	10	CG638372
CG136144 104_521.1	63	2	CG136144
BE043135 hk48d02.y	68	10	BE043135
CG479308 OST10037	68	10	CG479308
CG564040 OST187822	72	10	CG564040
AI650549 wa92d01.x	80	1	AI650549
CO745478 TGESt2yp0	71	7	CO745478
CG119567 104_496.1	79	10	CG119567
DR033729 5000G1E10	80	8	DR033729
BZ664011 SALK_0276	67	9	BZ664011
CG557728 OST174378	67	10	CG557728
CZ476204 d08233-5p	70	10	CZ476204
BU647204 1112056E0	77	5	BU647204
DR083206 PMU51-016	77	8	DR083206
DN337550 LTB3187-0	79	8	DN337550
CZ906313 BC0210 Sa	56	10	CZ906313
AI536756 tol3a03.x	61	1	AI536756
AI795111 sb76909.y	64	1	AI795111
BQ100258 ph74606.y	73	3	BQ100258
CB832486 SWBmFCAV	73	6	CB832486
AL195007 Tetraodon	73	10	CNS02FGM
CAW90683 fdb0001f2	75	10	CAW90683
AA625835 zv87c11.8	79	1	AA625835
AA227334 z17b11.r	43	1	AA227334
BX946078 Arabidops	50	10	BX946078
CA587101 LBG27046	53	6	CA587101
AI582356 tq67b05.x	64	1	AI582356
AI094171 qa29a09.9	70	1	AI094171
AI554288 tq05d02.x	73	1	AI554288
CL303202 P019A02 G	73	10	CL303202
CG729734 1119114D0	74	10	CG729734
AA017154 z841c01.8	76	1	AA017154
BQ269183 ik22c02.y	78	3	BQ269183
CL213371 A046E05 G	79	10	CL213371
AA097244 mm35b10.x	80	1	AA097244
CN922421 000410AEL	51	7	CN922421
BZ354994 SALK_1262	60	9	BZ354994
AL797821 AL797821	61	1	AL797821
AI569396 tm86a08.x	64	1	AI569396
CG638918 OST369134	66	10	CG638918
DQ041915 Homo sapi	68	11	DQ041915
DQ041916 Pan trogl	68	11	DQ041916
BX690564 BX690564	5	5	BX690564
DR108645 JHU168E11	69	8	DR108645
CV307374 tJ43d06.b	77	7	CV307374
CC325376 TEA231 Ba	77	9	CC325376
CC883422 SALK_0942	79	1	CC883422
CA586216 LBC01186	45	9	CA586216
CA587090 LBG27p33	49	6	CA587090
AZ817412 2M0086J11	57	9	AZ817412
AI318464 fa08h04.x	60	1	AI318464
CG631433 OST347814	61	10	CG631433
AZ767834 IM0567Q03	62	9	AZ767834
CR064445 Forward s	62	11	CR064445
AA706076 ah25h02.8	65	1	AA706076
BH000484 2M0288D24	66	9	BH000484
CZ483689 f01213-5p	67	10	CZ483689
CZ488696 f06057-5p	67	10	CZ488696
BX189635 Danilo rer	68	10	BX189635
BX128997 Danilo rer	69	10	BX128997
BJ036111 BJ036111	70	3	BJ036111
AI826111 wk28901.x	71	1	AI826111
BH217655 1006057D1	71	9	BH217655
CR085416 Reverse s	71	11	CR085416
CG526501 OST103143	72	10	CG526501
CK725806 SWBbL3CAW	73	7	CK725806
AA136590 zn95c03.s	74	1	AA136590
CG869661 XR0120 Sa	75	10	CG869661
H74365 269 Deletio	78	8	H74365
H42857 yo10e01.e1	79	8	H42857

96 18.2 11.1 80 10 CZ471354 CZ471354 d00057-3p  
 97 18.2 11.1 80 11 DE059536 DE059536 Oryzias 1  
 98 11.0 48 10 CZ459338 CZ459338 c04546-5p  
 99 11.0 50 10 CZ475687 CZ475687 d07366-5p  
 c 100 11.0 52 9 AZ584594 AZ584594 IM0389A14

## ALIGNMENTS

RESULT 1  
 CF981901/c  
 LOCUS  
 DEFINITION maj75a12.y1 McCarrey Eddy 18 day preleptotene spermatocytes Mus  
 musculus CDNA clone IMAGE:7031702 5', mRNA sequence.  
 CF981901  
 ACCESSION  
 VERSION CF981901.1 GI:38514950  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 50)

REFERENCE  
 AUTHORS McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,  
 Martin, J., Wylie, T., Dantes, M., Bowers, Y., Theising, B., Gibbons, M.,  
 Ritter, E., Tsagareishvili, R., Ronko, I., Maguire, L., Kennedy, S.,  
 Bennett, J., Waterston, R. and Wilson, R.

TITLE  
 JOURNAL  
 COMMENT  
 NIEHS Mouse  
 Unpublished (2002)  
 Contact: McCarrey/Eddy NIEHS Mouse  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Library constructed and donated by J. McCarrey, Ph.D. (Southwest  
 Foundation for Biomedical Research, Dept. of Genetics) - excision  
 done by E.M. Eddy, Ph.D. (National Institutes of Health, National  
 Institute of Environmental Health Sciences).  
 Seq primer: Primer name ambiguous.

FEATURES  
 source

1..50  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:7031702"  
 /sex="male"  
 /tissue\_type="18-day preleptotene spermatocytes"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="McCarrey Eddy 18 day preleptotene  
 spermatocytes"  
 /note="Organ: testis; Vector: pBluescript SK+  
 (Stratagene); Site 1: XhoII; Site 2: EcoRI; cDNA oligo  
 dt-primed [5'-(GA)10-ACTAGTCGAGTTTCTTTT-3'] and  
 directionally cloned using 5' linkers 5'-AATTCGACGAG-3'  
 and 5'-CTCGTCCG-3'. Size selection of >400bp material  
 gives average insert size ranging from 1-2 kb. Library was  
 mass excised (from lambda-UniZAP-XR) and resulting  
 single-stranded phagemids were prepped and transformed into  
 DH10B. Library constructed and donated by J. McCarrey,  
 Ph.D. (Southwest Foundation for Biomedical Research, Dept.  
 of Genetics); excision done by E.M. Eddy, Ph.D. (National  
 Institutes of Health, National Institute of Environmental  
 Health Sciences)."

ORIGIN

Query Match 14.1%; Score 23.2; DB 7; Length 50;  
 Best Local Similarity 70.5%; Pred. No. 2.1e+04;  
 Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 80 GACTGTCTTACCCCGGGAGGAGTGACGACGAGTCCAAAGCCC 123

Db 44 GCTAGTCTTACCCCGGGAGGATGCAGTCAGACCGCACCAAGCCC 1

RESULT 2  
 CL639648/c

LOCUS  
 DEFINITION P028B09 GGTc Gene Trap Library GV08C05 Mus musculus CDNA clone  
 P028B09, mRNA sequence.

ACCESSION  
 VERSION CL639648  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 58)

REFERENCE  
 AUTHORS Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,  
 Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
 A large-scale, gene-driven mutagenesis approach for the functional  
 analysis of the mouse genome  
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
 12904583

COMMENT  
 On Mar 22, 2005 this sequence version replaced gi:58225660.  
 Contact: GGTc  
 German Genetrap Consortium (GGTC)

Email: info@genetrap.de  
 FlipROSAbetago gene trap. Sequence tag generated by 5'RACE.  
 Additional sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?'  
 clone\_id=P028B09' ES cell line harboring insertion mutation of  
 target gene is available at:  
 'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
 1' Inhouse Sequence Identifier: 19838  
 Class: Gene Trap.

FEATURES  
 source

1..58  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"  
 /clone="P028B09"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
 /clone\_lib="GGTC Gene Trap Library GV08C05"  
 /note="Vector: FlipROSAbetago"

ORIGIN

Query Match 14.1%; Score 23.2; DB 10; Length 58;  
 Best Local Similarity 65.4%; Pred. No. 2.2e+04;  
 Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 71 TCTGTGTTTGACTGTCTTACCCCGGGAGGAGTGACGACGAGTCCAAAGCCC 122

Db 53 TCTGCAGAACATGCTTAATTCGCGCAGCGGGGAGCAGGTGCCAGCCC 2

RESULT 3

LOCUS  
 DEFINITION AZ791987/c

2M0043G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0043G08 F, genomic survey sequence.

ACCESSION  
 VERSION AZ791987  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 71)





```

ORIGIN
Query Match      12.9%; Score 21.2; DB 7; Length 72;
Best Local Similarity 60.3%; Pred. No. 9.8e+04;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 40 CAGTCCGAGTCTCTCAAGGCACAGGTCTCTTCTGTTGACTGTCTTACCCCGG 97
Db 65 CAGTGAAGCATCTCTTCAGAGTCTGAAGTCTATCTGCTGTGAAAGTCTGACGACGAG 8

RESULT 6
BJ083039/c
LOCUS
DEFINITION
BJ083039 NIBB Mochii normalized xenopus tailbud library Xenopus
laevis cDNA clone XL083017 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 66)
REFERENCE
1 Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
Kohara,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
FEATURES
source
Location/Qualifiers
1..66
/mol_type="mRNA"
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL083017"
/tissue_type="whole embryo"
/dev stage="stage 25"
/clone.lib="NIBB Mochii normalized Xenopus tailbud
library"

ORIGIN
Query Match      12.7%; Score 20.8; DB 3; Length 66;
Best Local Similarity 60.7%; Pred. No. 1.3e+05;
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 107 CAGCAGCTGACGCCCCAGTGAAGACATCTGAGCTCAATCCAGATAAGTGA 162
Db 61 CATCAACCTATTCTAGCCAAATGTGATGATACATCTGCTTTACCTCGACATATGTA 6

RESULT 7
H84929/c
LOCUS
DEFINITION
H84929 Y85101.s1 Soares melanocyte 2N5HM Homo sapiens cDNA clone
IMAGE:249553 3', similar to gb:Z22548 THIOI-SPECIFIC ANTIOXIDANT
PROTEIN (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
H84929.1 GI:1064424
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 75)
REFERENCE
1 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,P.,
Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
1..75
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3867259"
/db_xref="taxon:9606"
/clone="IMAGE:249553"
/sex="Male"
/tissue_type="melanocyte"
/lab host="DH10B (ampicillin resistant)"
/clone.lib="Soares melanocyte 2N5HM"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN
Query Match      12.7%; Score 20.8; DB 8; Length 75;
Best Local Similarity 58.6%; Pred. No. 1.3e+05;
Matches 34; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 72 CCTGTTTGAATGTCCTTACCCGGGAGGCGAGTGCAGCCAGCTGCAAGCCCAAGT 129
Db 72 CCTGTTTGAATGTCCTTACCCGGGAGGCGAGTGCAGCCAGCTGCAAGCTGCGAGT 15

RESULT 8
AZ768319/c
LOCUS
DEFINITION
AZ768319 Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0568E17 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ768319.1 GI:12887304
Mus musculus (house mouse)
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 67)
REFERENCE
1 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```

**TITLE**  
Niederhausern, A. and Wright, D., Weiss, R.  
**JOURNAL**  
Mouse whole genome scaffolding with paired end reads from 10kb  
**COMMENT**  
Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0568 row: E column: 17  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 67.

# FEATURES

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Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0568E17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells, and selected for ampicillin resistance."

# ORIGIN

Query Match 12.6%; Score 20.6; DB 9; Length 67;  
Best Local Similarity 62.7%; Pred. No. 1.5e+05;  
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 21 GGGACTGGCAGTTCAGACGTCGCGAGTTCCTCAAGGACAGGTCCTCTT 71  
|||||  
DB 52 GGGACAGCCCATCTCTAGTCGAGATGCAATACCTCAATATCATGTATCTT 2  
|||||

RESULT 9  
CL603643/c  
LOCUS  
DEFINITION  
CH240\_178P06.TV CHORI-240 Bos taurus genomic clone CH240\_178P06,  
genomic survey sequence.  
ACCESSION  
CL603643  
VERSION  
CL603643.1 GI:48871675  
KEYWORDS  
GSS.  
SOURCE  
Bos taurus (cow)  
ORGANISM  
Bos taurus

REFERENCE  
AUTHORS  
TITLE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Fecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 74)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

# JOURNAL COMMENT

CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_178P06.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acaetano@embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 178 row: P column: 06  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 74.

# FEATURES

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/organism="Bos taurus"  
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/db\_xref="taxon:9913"  
/clone="CH240\_178P06"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

# ORIGIN

Query Match 12.6%; Score 20.6; DB 10; Length 74;  
Best Local Similarity 47.8%; Pred. No. 1.5e+05;  
Matches 32; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 89 TACCCGGGGAGGAGTGCAGCCAGCTGCAAGCCCAAGTCAAGACATCTGAGCTCA 148  
|||||  
DB 74 TAACCGTGAAGAAGAGAGAGCGAAAGCAANNNNNNNNNNNGAAGATATAAGNNNNNA 15  
|||||

QY 149 ATCCAGA 155  
|||||

DB 14 ATGCAGA 8  
|||||

RESULT 10  
DQ051485/c

LOCUS  
DEFINITION  
Pan troglodytes SOD3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
DQ051485  
VERSION  
DQ051485.1 GI:66904687  
KEYWORDS  
GSS.

SOURCE  
Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes

REFERENCE  
AUTHORS  
TITLE  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Pan.  
1 (bases 1 to 80)

REFERENCE  
AUTHORS  
TITLE  
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,  
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Cividello, D.,  
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.  
A Scan for Positively Selected Genes in the Genomes of Humans and

```

Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
15869325
REFERENCE
2 (bases 1 to 80)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source
1..80
/organism="Pan troglodytes"
/mol_type="genomic DNA"
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<1..>80
/gene="SOD3"
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ORIGIN
Query Match 12.6%; Score 20.6; DB 11; Length 80;
Best Local Similarity 67.4%; Pred. No. 1.6e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 122 CCCACAGTGAAGACATCTGAGCTCAATCAATCCAGTAAGTGACA 164
|||||
Db 72 CCCACCGTGAAGATCCCAATGAGATCATCACTGCCCGCATGTGACA 30
|||||

RESULT 11
AZ829920/c
LOCUS
DEFINITION
2M0107A19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0107A19 R, genomic survey sequence.
ACCESSION
AZ829920
VERSION
AZ829920.1 GI:12999828
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 60)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: A column: 19
Seq primer: CACACGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 60.
FEATURES
source
1..60
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0107A19"

Chimpanzees
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 12.4%; Score 20.4; DB 9; Length 60;
Best Local Similarity 61.1%; Pred. No. 1.7e+05;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 108 AGCCAGCTGCAGCCGCCAGTGAAGACATCTGAGCTCAATCCAGTAAGTG 161
|||||
Db 57 AGTAAAGTGTAGCTTGCAGGCACGAGCATCTGAGTCAAGCCCAAGAAAGAG 4
|||||

RESULT 12
AA917946
LOCUS
DEFINITION
79 bp mRNA linear EST 17-APR-1998
ol68g04.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534806 3',
similar to TR:Q07611 Q07611 PROLINE-RICH PROTEOLYCAN PRPG2.
;contains MSRI.t3 MSRI repetitive element ;, mRNA sequence.
ACCESSION
AA917946
VERSION
AA917946.1 GI:3057836
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 79)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1534806"
/lab_host="DH10B"

```

/clone\_lib="NCI\_CGAP\_Kid3"  
 /note="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 12.4%; Score 20.4; DB 1; Length 79;  
 Best Local Similarity 65.2%; Pred. No. 1.8e+05;  
 Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 27 GGCAGTTCCTAGACAGTCCGAGTCTCTCAAGGCACAGGTCTCTTC 72  
 |||||  
 Db 9 GGACCTTGCTCCACATCCCACTCCCTCGGAGGCGCCCTTC 54  
 |||||

## RESULT 13

CG869849/c  
 LOCUS  
 DEFINITION XS0340 Sanger Institute Gene Trap Library pGT01xf Mus musculus cDNA, mRNA sequence.

ACCESSION CG869849  
 VERSION CG869849.2 GI:60335575  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 57)

## REFERENCE

AUTHORS Sanger Institute Gene Trap Resource - SIGTR.

## TITLE

http://www.sanger.ac.uk/PostGenomics/genetraps/

## JOURNAL

Unpublished (2003)

## COMMENT

On Feb 25, 2005 this sequence version replaced gi:38533529.  
 Contact: Sanger Institute Gene Trap Resource - SIGTR  
 Wellcome Trust Sanger Institute  
 Email: info.genetraps@sanger.ac.uk  
 Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from  
 http://www.sanger.ac.uk/PostGenomics/genetraps/  
 Class: Gene Trap.

## FEATURES

source

1..57  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 OLA"  
 /db\_xref="taxon:10090"  
 /sex="Male"  
 /cell\_type="Embryonic Stem Cell"  
 /clone\_lib="Sanger Institute Gene Trap Library pGT01xf"  
 /note="Vector: pGT01xf"

## ORIGIN

Query Match 12.3%; Score 20.2; DB 10; Length 57;  
 Best Local Similarity 59.6%; Pred. No. 1.9e+05;  
 Matches 34; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 39 ACAGTCCGAGTTCACAGGCACAGTCTCTCTCGTTTACTGCTCTTACCTTACCCCG 95  
 |||||  
 Db 57 AAAACCCCGATCTGCTGAGGCACAGCCCGGAGGTGGGAGGTCTCTTCCCG 1  
 |||||

## RESULT 14

CL640815/c  
 LOCUS  
 DEFINITION M079807 GGTc Gene Trap Library GV07C04 Mus musculus cDNA clone

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

M079807, mRNA sequence.

CL640815 GI:61683779  
 GSS.  
 Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 74)

TITLE

A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome  
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)

JOURNAL

PUBMED

COMMENT

On Mar 22, 2005 this sequence version replaced gi:49489262.

Contact: GGTc

German Genetraps Consortium (GGTC)

Email: info@genetraps.de

U3CEO gene trap. Sequence tag generated by 5' RACE. Additional

sequence information can be found at:

'http://genetraps.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=M079807' ES cell line harboring insertion mutation of

target gene is available at:

'http://genetraps.gsf.de/project/web\_new/order\_clones/howtoorder.htm'

1' Inhouse Sequence Identifier: 14819

Class: Gene Trap.

Location/Qualifiers

1..74

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129 Sv"

/db\_xref="taxon:10090"

/clone="M079807"

/sex="Male"

/cell\_type="Embryonic stem cell"

/cell\_line="ES cells 129S2 (formerly 129/SvPas)"

/clone\_lib="GGTC Gene Trap Library GV07C04"

/note="Vector: U3CEO"

Query Match 12.3%; Score 20.2; DB 10; Length 74;

Best Local Similarity 63.3%; Pred. No. 2.1e+05;

Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 116 GCAAGCCCCACAGTCAAGACATCTGAGCTCAATCCAGATGACACA 164  
 |||||

Db 60 GTAAGACACTTGTAAGAAGAACTGAAGACATTTACAGATAACACAGA 12  
 |||||

AKI98748

AKI98748.1 GI:56022925

HTC; ASSETS.

Mus musculus (house mouse)

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1

Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,

Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,

Hayashizaki, Y. and Carninci, P.

Libraries enriched for alternatively spliced exons reveal splicing

patterns in melanocytes and melanomas

Nat. Methods 1, 233-239 (2004)

2 (bases 1 to 77)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1

Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,

Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,

Hayashizaki, Y. and Carninci, P.

Libraries enriched for alternatively spliced exons reveal splicing

patterns in melanocytes and melanomas

Nat. Methods 1, 233-239 (2004)

## AUTHORS

Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,  
Hori,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,  
Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watahiki,A. and  
Hayashizaki,Y.

## Direct Submission

Submitted (15-SEP-2004) Yoshihide Hayaishizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa, 230-0045, Japan (E-mail:genome-res@gscl.riken.jp,  
URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

Alternative Splicing Libraries (ASLs) are prepared by: Preparing  
of single-stranded DNA using a RNA template from full length cDNA  
libraries, hybridizing of  
single-stranded DNAs, removing of remaining single-stranded DNA,  
digesting of regions comprising double-stranded DNA by a set of 4  
bp-cutters, capturing of DNA hybrids with loop structures  
(alternative spliced exon), ligating of Y-shaped primers to  
isolated DNA hybrids with loop structures, PCR amplification of  
ligation products and their cloning into pFLCI vector. (Reference).

## FEATURES

source

```
1. .72
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="YIG0129B02"
/cell_line="mixture of B16-F10Y and melan-c"
/cell_type="mixture of melanoma cell and melanocyte cell"
/clone_lib="Alternative Splicing Library L1"
/notes="strand:minus, reference:ENSEMBL:Mouse-Transcript-
ENST:ENSMUST0000002683, based on BLAT search"
```

## ORIGIN

```
Query Match 12.3%; Score 20.2; DB 4; Length 77;
Best Local Similarity 63.3%; Pred. No. 2.1e+05;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 3 TCGGCCACCTTGTATGAGGGACATGGGAGCTTCTAGACATCCGAGCT 51
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 TCGGCCATCTCGTGGAGACACCGCTGCTGATTTCTACTGTGCGGAGT 71
```

## RESULT 16

```
BG237470
LOCUS
DEFINITION
BG237470 72 bp mRNA linear EST 23-JUL-2004
sab07a06.y1 Gm-cl071 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl071-780 5', mRNA sequence.
```

```
ACCESSION
BG237470
VERSION
BG237470.1 GI:12772616
```

## KEYWORDS

EST.

## SOURCE

Glycine max (soybean)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,  
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,  
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,  
Schurr,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.

## TITLE

JOURNAL

COMMENT

Public Soybean EST Project  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this  
clone is listed in the 'Other ESTs on clone' field. Putative full  
length read vector to vector length is 81. This clone is available  
through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA  
(phone: 800 423 4163; email: info@biogeneticservices.com).

## FEATURES

source

```
1. .72
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl071-780"
/tissue_type="immature pods (~2cm long) of greenhouse
grown plants"
/lab_host="DH10B"
/clone_lib="Gm-cl071"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; The
cDNA library was constructed from mRNA isolated from
immature pods (approximately 2cm long) of greenhouse grown
plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a NotI restriction site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-SalI restriction
site of the pSPORT1 vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
Urbana-Champaign. email: l-vodkin@uiuc.edu"
```

## ORIGIN

```
Query Match 12.2%; Score 20; DB 2; Length 72;
Best Local Similarity 58.3%; Pred. No. 2.4e+05;
Matches 35; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 47 GAAGTCTCAAGGCACAGGTCTCTCTGCTTGACTGTCTTACCCCGGAGGAGTG 106
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 GAAATCTCAAGGAAAGCCCTCTTGTGTTCTACCGAACTAAACTAATAAGAAGTG 72
```

## RESULT 17

```
AF149527
LOCUS
DEFINITION
AF149527 Human chromosome 18q21 from exon-trapping Homo sapiens
Genomic clone lp18, genomic survey sequence.
```

```
ACCESSION
AF149527.1 GI:8485853
```

## KEYWORDS

GSS.

## SOURCE

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS

Chen,H., Huo,Y., Patel,S., Zhu,X., Swift-Scanlan,T., Reeves,R.H.,  
DePaulo,R. Jr., Ross,C.A. and McInnis,M.G.  
Gene identification using exon amplification on human chromosome  
18q21: implications for bipolar disorder

## JOURNAL

PUBMED

COMMENT

11032383  
Contact: Chen H  
Psychiatry and Behavioral Sciences  
Johns Hopkins University School of Medicine  
600 N. Wolfe Street, Baltimore, MD 21287, USA  
Email: hc@welchlink.welch.jhu.edu  
Class: exon-trapped.

## FEATURES

source

```
1. .64
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
```

```

/clip="18q21"
/clone="1p18"
/clone_lib="Human chromosome 18q21 from exon-trapping"

ORIGIN
Query Match 12.1%; Score 19.8; DB 9; Length 64;
Best Local Similarity 69.2%; Pred. No. 2.7e+05;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 95 GGGAGGAGTGGCAGCAGTGGCAAGCCCAAGTGAAG 133
|||||
DB 22 GAGGATCCCAAGCAGCCTGTGGGAAGCCACGCGTGAAG 60
|||||

RESULT 18
AZ615721/c
LOCUS
DEFINITION
1M0445N01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0445N01 F, genomic survey sequence.
ACCESSION
AZ615721
VERSION
AZ615721.1 GI:11737827
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0445 row: N column: 01
Seq primer: CGTTGTAACACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 77.
Location/Qualifiers
1. .77
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0445N01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

```

```

purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 12.1%; Score 19.8; DB 9; Length 77;
Best Local Similarity 63.8%; Pred. No. 2.8e+05;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 96 GGGAGGAGTGGCAGCAGTGGCAAGCCCAAGTGAAGACATCTGA 142
|||||
DB 63 GGCAGACAGTCCAGAAAGATGCCCAAGCCACAGCTACTACATCAGA 17
|||||

RESULT 19
AG829487
LOCUS
DEFINITION
80 bp DNA linear GSS 01-DEC-2004
Sus scrofa DNA, BAC clone L243P12, shotgun sequence of subclone
L243P12S002E03, read with -21M13 primer, genomic survey sequence.
ACCESSION
AG829487
VERSION
AG829487.1 GI:56375985
KEYWORDS
GSS.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1
Tanaka, M., Suzuki, K., Morozumi, T., Kobayashi, E., Matsumoto, T.,
Domukai, M., Eguchi-Ogawa, T., Shinkai, H., Awata, T. and Uenishi, H.
Genomic structure of the distal extended-class II region in swine
Unpublished
2 (bases 1 to 80)
Uenishi, H., Tanaka, M. and Awata, T.
Direct Submission
Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
Agrobiological Sciences, Animal Genome Laboratory, Genome Research
Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
(E-mail: huenishi@affrc.go.jp, Tel: 81-29-838-8627,
Fax: 81-29-838-8627)
Correspondence to:
Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department, National
Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
Tel: +81-29-838-8627
Fax: +81-29-838-8627
e-mail: huenishi@affrc.go.jp
Sequencing was carried out in Animal Genome Research Program
(Japan)
by National Institute of Agrobiological Sciences
and STAFF-Institute.
Subclones of BAC clones were constructed with pUC18 vector.
Basecalling was performed by Phred 0.020425.c.
Vector sequences were eliminated by crossmatch version 0.990319.
Low quality bases were trimmed based on the quality values with the
aid of the trim-alt option of Phred.
Location/Qualifiers
1. .80
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="L243P12"
/sub_clone="L243P12S002E03"
/clone_lib="Sus scrofa shotgun BAC sequence"

ORIGIN
Query Match 12.1%; Score 19.8; DB 10; Length 80;
Best Local Similarity 77.4%; Pred. No. 2.8e+05;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 79 TGACTGTCTTACCCCGGGAGGAGGTGCAG 109

```





[illegible]

ORGANISM	Trypanosoma brucei
Source	Trypanosoma brucei

REFERENCE  
AUTHORS

1 (bases 1 to 59)  
Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S. E., Rajandream, M. A. and Barrell, B. G.

Submitted (10 Dec 2007) *Myxobolus* strain genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of

to give a tight size distribution (mean = 10.1) was mechanically sheared to 4 kb). The  $v + 1$  method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsaved@tigr.org

```

email: nersayev@qcd.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
            Location/Qualifiers
                1..59
                    /organism="Trypanosoma brucei"
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/clone="112c05"
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RESULT 25  
CG638372  
OCUC  
DEFINITION  
CG638372 62 bp mRNA linear GSS 02-OCT-2003  
OST367812 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST367812,  
mRNA sequence.  
CG638372  
CG638372.1 GI:37462221  
VERSION

**SOURCE** : Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 62)

REFERENCE  
AUTHORS  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.  
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
14610273

TITLE  
JOURNAL  
PUBMED  
COMMENT  
Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
Location/Qualifiers  
1..62  
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/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST367812"  
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Best Local Similarity 64.4%; Pred. No. 3.5e+05;  
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
Qy 65 GTCTCTTCCTGGTTGACTGCTTACCCGGGAGGACGTGCAG 109  
Db 16 GTGTGTACTGGTTTGCTTCACGTCGCCATGGAAGCCAGAAGAG 60

Search completed: March 3, 2006, 11:01:18  
Job time : 8979.05 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds  
(without alignments)  
2714.499 Million cell updates/sec

Title: US-10-655-801-19  
Perfect score: 18  
Sequence: 1 catcaagggtgcccagaga 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5983141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	76.7	47	6	E07475
C 2	13.8	76.7	74	15	AJ525630 Arabidops
C 3	13.4	74.4	39	6	QO801018 Sequence
C 4	13.4	74.4	44	6	AX206894 Sequence
C 5	13.4	74.4	45	6	AX146612 Sequence
C 6	13.4	74.4	65	6	CQ532654 Sequence
C 7	13.2	73.3	23	2	CEL487557
C 8	13.2	73.3	23	2	AJ421757 Drosophila
C 9	13.2	73.3	23	2	DME421758
C 10	13.2	73.3	23	6	CQ873596 Sequence
C 11	13.2	73.3	51	6	CQ006930 Sequence
C 12	13.2	73.3	68	6	AX233504 Sequence
C 13	13.2	73.3	76	6	CQ874036 Sequence
C 14	13.2	73.3	80	9	S76293 Hox-A Hox-1
C 15	13	72.2	18	6	AR086069 Sequence
C 16	13	72.2	18	6	AR140423 Sequence
C 17	13	72.2	18	6	AR146904 Sequence
C 18	13	72.2	33	8	HSA403872 Homo sapi

AX727459 Sequence	17	12.8	71.1	6	AX727459
AR164017 Sequence	20	12.8	71.1	6	AR164017
AX059371 Sequence	21	12.8	71.1	6	AX059371
CQ890713 Sequence	22	12.8	71.1	6	CQ890713
CQ897253 Sequence	23	12.8	71.1	6	CQ897253
CQ898402 Sequence	24	12.8	71.1	6	CQ898402
AX206899 Sequence	25	12.8	71.1	6	AX206899
AX931869 Sequence	26	12.8	71.1	6	AX931869
E11529 PCR primer	27	12.8	71.1	37	E11529
E07474 Oligonucleo	28	12.8	71.1	38	E07474
A22368 oligonucleo	29	12.8	71.1	52	A22368
AR076116 Sequence	30	12.8	71.1	52	AR076116
M26824 Mouse Ig un	31	12.8	71.1	57	M26824
CQ553838 Sequence	32	12.8	71.1	60	CQ553838
CQ531035 Sequence	33	12.8	71.1	65	CQ531035
CQ534516 Sequence	34	12.8	71.1	65	CQ534516
CQ554931 Sequence	35	12.8	71.1	65	CQ554931
CQ556308 Sequence	36	12.8	71.1	65	CQ556308
CS110174 Sequence	37	12.8	71.1	75	CS110174
AR571546 Sequence	38	12.4	68.9	19	AR571546
AX129656 Sequence	39	12.4	68.9	19	AX129656
BD133801 ChimERIC	40	12.4	68.9	20	BD133801
AX469759 Sequence	41	12.4	68.9	20	AX469759
AR217119 Sequence	42	12.4	68.9	24	AR217119
AX099239 Sequence	43	12.4	68.9	24	AX099239
AR028551 Sequence	44	12.4	68.9	27	AR028551
AX206898 Sequence	45	12.4	68.9	32	AX206898
AX828628 Sequence	46	12.4	68.9	33	AX828628
AX551668 Arabidops	47	12.4	68.9	39	AX551668
CS000192 Sequence	48	12.4	68.9	40	CS000192
AR217113 Sequence	49	12.4	68.9	45	AR217113
CQ001515 Sequence	50	12.4	68.9	51	CQ001515
CQ005999 Sequence	51	12.4	68.9	51	CQ005999
CQ537961 Sequence	52	12.4	68.9	60	CQ537961
CQ979038 Sequence	53	12.4	68.9	77	CQ979038
AR160928 Sequence	54	12.2	67.8	20	AR160928
CQ878663 Sequence	55	12.2	67.8	20	CQ878663
AR473981 Sequence	56	12.2	67.8	20	AR473981
AX448320 Sequence	57	12.2	67.8	20	AX448320
AX664291 Sequence	58	12.2	67.8	21	AX664291
CQ793286 Sequence	59	12.2	67.8	21	CQ793286
AR612404 Sequence	60	12.2	67.8	22	AR612404
AX342375 Sequence	61	12.2	67.8	22	AX342375
BD142821 Method of	62	12.2	67.8	24	BD142821
AX446606 Sequence	63	12.2	67.8	24	AX446606
A2595 Sequence 11	64	12.2	67.8	30	A2595
A88783 Sequence 93	65	12.2	67.8	30	A88783
AR149763 Sequence	66	12.2	67.8	30	AR149763
BD066296 An antise	67	12.2	67.8	30	BD066296
BD130647 Aiolos ge	68	12.2	67.8	30	BD130647
AR285590 Sequence	69	12.2	67.8	30	AR285590
AR404882 Sequence	70	12.2	67.8	30	AR404882
AR654614 Sequence	71	12.2	67.8	30	AR654614
BD225214 Orphan nu	72	12.2	67.8	34	BD225214
AX339454 Sequence	73	12.2	67.8	34	AX339454
CQ002546 Sequence	74	12.2	67.8	50	CQ002546
CQ808850 Sequence	75	12.2	67.8	50	CQ808850
CQ007506 Sequence	76	12.2	67.8	51	CQ007506
AX204242 Sequence 2	77	12.2	67.8	51	AX204242
BD194944 86 human	78	12.2	67.8	53	BD194944
CQ855463 Sequence	79	12.2	67.8	59	CQ855463
CQ537531 Sequence	80	12.2	67.8	60	CQ537531
CQ539496 Sequence	81	12.2	67.8	60	CQ539496
CQ555569 Sequence	82	12.2	67.8	65	CQ555569
AX187656 Sequence	83	12.2	67.8	77	AX187656
CQ874790 Sequence	84	12.2	67.8	77	CQ874790
AX328457 Sequence	85	12	66.7	28	AX328457
CQ848157 Sequence	86	12	66.7	30	CQ848157
CS122771 Sequence	87	12	66.7	48	CS122771
CQ008400 Sequence	88	12	66.7	48	CQ008400
AX160392 Sequence	89	12	66.7	50	AX160392
AX160391 Sequence	90	12	66.7	50	AX160391
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c 92 12 66.7 60 6 CQ538792 Sequence
c 93 12 66.7 65 6 CQ552279 Sequence
c 94 11.8 65.6 17 6 BD241406 Methods a
11.8 65.6 17 6 CQ622510 Sequence
96 11.8 65.6 17 6 CQ622511 Sequence
97 11.8 65.6 17 6 CQ622512 Sequence
98 11.8 65.6 17 6 AR466573 Sequence
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100 11.8 65.6 17 6 AR466575 Sequence

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## ALIGNMENTS

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RESULT 1
LOCUS E07475 47 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotides for PCR probe.
ACCESSION E07475
VERSION E07475.1 GI:2175613
KEYWORDS JP 1994133780-A/6.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Negoro, T. and Tanaka, N.
TITLE NEW MODIFIED T-PA
JOURNAL Patent: JP 1994133780-A 6 17-MAY-1994;
SUMITOMO PHARMACEUT CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994133780-A/6
PD 17-MAY-1994
PF 23-OCT-1992 JP 1992309285
PI NEGORO TAKATSU, TANAKA NAOMI
PC C12N15/58,A61K37/54,C07K15/06,C07K15/14,C12N1/21, PC
C12N5/10//C12P21/02,
PC (C12N1/21,C12R1:19), (C12N5/10,C12R1:91), (C12P21/02,C12R1:19),
PC (C12P21/02,
PC (C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key
FT source 1..47
FT misc_feature 1..47 /organism='Artificial sequences' FT
FT /note='Oligonucleotide IKGR'.
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/organism="unidentified"
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Db 39 CATCAAGGCGCCTAG 23
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RESULT 2
LOCUS ATH525630 74 bp DNA linear PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 101G06.
ACCESSION AJ525630
VERSION AJ525630.1 GI:26793866

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KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Leclercq, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 74)
AUTHORS Balzerque, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

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FEATURES
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left border"

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Qy 1 CATCAAGGCGCCGAGA 18
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Db 24 CATCACACGTGGCCGNGA 41
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RESULT 3
LOCUS CQ801018/c 39 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 9 from Patent WO2004033728.
ACCESSION CQ801018
VERSION CQ801018.1 GI:47057790
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM

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```

REFERENCE 1
AUTHORS van Dongen, J.J., Langerak, A.W., Schuurink, E.M., van Miquel, J.F., garzia Sanz, R., Parreira, A., Smith, J.L., Lavender, F.L., Morgan, G.J., Evans, P.A., Kneba, M., Hummel, M., Macintyre, E.A. and Bastard, C.
TITLE Nucleic acid amplification primers for pcr-based clonality studies
JOURNAL Patent: WO 2004033728-A 9 22-APR-2004;
Erasmus Universiteit Rotterdam (NL); Van Dongen, Jacobus, Johannes, Maria (NL)
FEATURES
source
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Location/Qualifiers

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/organism="synthetic construct"
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAAAGGTGGCCGAG 17
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Db 32 TCAAAGGGGCCGAG 18

RESULT 4
AX206894/c
LOCUS AX206894 44 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 2 from Patent WO015429.
ACCESSION AX206894
VERSION AX206894.1 GI:15394705
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mattanovich,D., Katinger,H., Hohenblum,H., Naschberger,S. and Weik,R.
TITLE Method for the manufacture of recombinant trypsin
JOURNAL Patent: WO 015429-A 2 02-AUG-2001;
POLYMER Scientific Immunobiologische Forschung GmbH (AT)
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAAGGTGGCCG 15
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Db 38 CATCAAAGGGGCCG 24

RESULT 5
AX146612
LOCUS AX146612 45 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 74 from Patent WO0134654.
ACCESSION AX146612
VERSION AX146612.1 GI:14285005
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Strauch,K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 74 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES
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            /db_xref="taxon:9606"

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Best Local Similarity 93.3%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
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Db 26 CCAAGGTGGCCGAGA 40

RESULT 6
CQ532654
LOCUS CQ532654 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 2289 from Patent WO0210449.
ACCESSION CQ532654
VERSION CQ532654.1 GI:41498918
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
PATENT: WO 0210449-A 2289 07-FEB-2002;
COMPUGEN INC. (US)
FEATURES
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Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
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Db 2 CAAAGTGGCCAAGA 16

RESULT 7
CEL487557/c
LOCUS CEL487557 23 bp RNA linear INV 09-OCT-2003
DEFINITION Caenorhabditis elegans microRNA mir-2.
ACCESSION AJ487557
VERSION AJ487557.2 GI:35210303
KEYWORDS microRNA; mir-2 gene; miRNA.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1
AUTHORS Lau,N.C., Lim,L.P., Weinstein,E.G. and Bartel,D.P.
TITLE An abundant class of tiny RNAs with probable regulatory roles in
JOURNAL Caenorhabditis elegans
PUBMED Science 294 (5543), 858-862 (2001)
REFERENCE 2
AUTHORS Bartel,D.P.
TITLE Direct Submision
JOURNAL Submitted (25-MAR-2002) Bartel D.P., Biology, MIT and Whitehead
INSTITUTE, 9 Cambridge Center, Cambridge, MA, 02142, USA
REMARK revised by [3]
REFERENCE 3 (bases 1 to 23)
AUTHORS Bartel,D.P.
TITLE Direct Submision
JOURNAL Submitted (16-SEP-2003) Bartel D.P., Biology, MIT and Whitehead
INSTITUTE, 9 Cambridge Center, Cambridge, MA, 02142, USA
COMMENT On Sep 25, 2003 this sequence version replaced gi:21212795.
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/organism="Drosophila melanogaster"
/notes="transcribed as larger precursor, predicted form
hairpin"

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Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
   |||||
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 8
DME421757/c
LOCUS      DME421757      23 bp      RNA      linear      INV 11-JUN-2003
DEFINITION Drosophila melanogaster microRNA mir-2a-1.
ACCESSION  AJ421757
VERSION     AJ421757.1 GI:17646042
KEYWORDS   miRNA.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 23)
            Lagos-Quintana M., Rauhut R., Lendeckel W. and Tuschl T.
            Identification of novel genes coding for small expressed RNAs
            Science 294 (5543), 853-858 (2001)
PUBMED     11679670
REFERENCE  2 (bases 1 to 23)
            Tuschl T.
            Direct Submission
            Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
            Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
            37077, Germany
COMMENT    Related sequences: AE003663.
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                        /chromosome="2L"
misc_RNA   1..23
            /notes="transcribed as larger precursor from the mir-2a-1
            gene, predicted to form hairpin"

ORIGIN
Query Match      73.3%; Score 13.2; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
   |||||
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 9
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LOCUS      DME421758      23 bp      RNA      linear      INV 11-JUN-2003
DEFINITION Drosophila melanogaster microRNA mir-2a-2.
ACCESSION  AJ421758
VERSION     AJ421758.1 GI:17646043
KEYWORDS   miRNA.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 23)
            Lagos-Quintana M., Rauhut R., Lendeckel W. and Tuschl T.
            Identification of novel genes coding for small expressed RNAs
            Science 294 (5543), 853-858 (2001)
PUBMED     11679670
REFERENCE  2 (bases 1 to 23)
            Tuschl T.
            Direct Submission
            Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
            Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
            37077, Germany
COMMENT    Related sequences: AE003663.
FEATURES   Location/Qualifiers
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                        /mol_type="other RNA"
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                        /chromosome="2L"
misc_RNA   1..23
            /notes="transcribed as larger precursor from the mir-2a-1
            gene, predicted to form hairpin"

ORIGIN
Query Match      73.3%; Score 13.2; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
   |||||
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 9
DME421758/c
LOCUS      DME421758      23 bp      RNA      linear      INV 11-JUN-2003
DEFINITION Drosophila melanogaster microRNA mir-2a-2.
ACCESSION  AJ421758
VERSION     AJ421758.1 GI:17646043
KEYWORDS   miRNA.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 23)
            Lagos-Quintana M., Rauhut R., Lendeckel W. and Tuschl T.
            Identification of novel genes coding for small expressed RNAs
            Science 294 (5543), 853-858 (2001)
PUBMED     11679670
REFERENCE  2 (bases 1 to 23)
            Tuschl T.
            Direct Submission
            Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
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            gene, predicted to form hairpin"

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Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 20 CATCAAGCTGGCTGTGA 3

RESULT 11
CQ006930
LOCUS      CQ006930      51 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 5570 from Patent WO0147944.

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Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 23)
Lagos-Quintana M., Rauhut R., Lendeckel W. and Tuschl T.
Identification of novel genes coding for small expressed RNAs
Science 294 (5543), 853-858 (2001)
PUBMED     11679670
REFERENCE  2 (bases 1 to 23)
            Tuschl T.
            Direct Submission
            Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
            Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
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COMMENT    Related sequences: AE003663.
FEATURES   Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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   |||||
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 10
CQ073596/c
LOCUS      CQ073596      23 bp      RNA      linear      PAT 27-SEP-2004
DEFINITION Sequence 15 from Patent WO2004076622.
ACCESSION  CQ073596
VERSION     CQ073596.1 GI:52747188
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
            Taira, K. and Kawasaki, H.
            Regulation of mammalian cells
            Patent: WO 2004076622-A 15 10-SEP-2004;
            National Institute of Advanced Industrial Science and Technology
            (JP)
FEATURES   Location/Qualifiers
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                        /mol_type="unassigned RNA"
                        /db_xref="taxon:9606"
misc_RNA   1..23
            /notes="transcribed as larger precursor from the mir-2a-2
            gene, predicted to form hairpin"

ORIGIN
Query Match      73.3%; Score 13.2; DB 6; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
   |||||
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 11
CQ006930
LOCUS      CQ006930      51 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 5570 from Patent WO0147944.

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ACCESSION      CQ006930
VERSION        CQ006930.1  GI:41013562
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1
AUTHORS        Shinkets,R.A. and Leach,M.
TITLE          Nucleic acids containing single nucleotide polymorphisms and
               methods of use thereof
JOURNAL        Patent: WO 0147944-A 5570 05-JUL-2001;
               Curagen Corporation (US)
FEATURES       Location/Qualifiers
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RESULT 12
AX233504/c
LOCUS          AX233504
DEFINITION     Sequence 147 from Patent WO0162788.
ACCESSION      AX233504
VERSION        AX233504.1  GI:15593016
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1
AUTHORS        Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.
TITLE          Corneodesmosin based test and model for inflammatory disease
JOURNAL        Patent: WO 0162788-A 147 30-AUG-2001;
               Oxagen Limited (GB)
FEATURES       Location/Qualifiers
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RESULT 13
CQ874036/c
LOCUS          CQ874036
DEFINITION     Sequence 455 from Patent WO2004076622.
ACCESSION      CQ874036
VERSION        CQ874036.1  GI:52747628
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE      1
AUTHORS        Taiza,K. and Kawasaki,H.
TITLE          Regulation of mammalian cells
JOURNAL        Patent: WO 2004076622-A 455 10-SEP-2004;
               National Institute of Advanced Industrial Science and Tec hnology
               (JP)
FEATURES       Location/Qualifiers
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RESULT 14
S76293
LOCUS          Hox-A|Hox-1 (clone 29c) 80 bp DNA linear ROD 05-MAY-2003
DEFINITION     Hox-A|Hox-1 (clone 29c) [rats, Sprague-Dawley, liver, Genomic, 80
ACCESSION      S76293
VERSION        S76293.1  GI:913078
KEYWORDS
SOURCE         Rattus sp.
ORGANISM       Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE      1 (bases 1 to 80)
AUTHORS        Sakoyama,Y., Mizuta,I., Ogasawara,N. and Yoshikawa,H.
TITLE          Cloning of rat homeobox genes
JOURNAL        Biochem. Genet. 32 (9-10), 351-360 (1994)
PUBMED        7702549
REMARK        GenBank staff at the National Library of Medicine created this
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QY      1 CATCAAAGTGGCCGAGA 18
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Db      2 CAACATAGTGGCCGAGA 19
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RESULT 15
AR086069
LOCUS          AR086069
DEFINITION     18 bp DNA linear PAT 07-SEP-2000

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DEFINITION Sequence 5146 from Patent WO03025176.
ACCESSION AX727459
VERSION AX727459.1 GI:30506802
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5146 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 87.5%; Pred. No. 2.4e+04;
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QY 2 ATCAAAGGTGGCGGAG 17
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RESULT 20
AR164017/c
LOCUS AR164017 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 216 from patent US 6271030.
ACCESSION AR164017
VERSION AR164017.1 GI:16234923
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 216 07-AUG-2001;
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Db 17 ATCAAACGTGGCTGAG 2
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LOCUS AX059371 20 bp DNA linear PAT 17-JAN-2001
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ACCESSION AX059371
VERSION AX059371.1 GI:12311476
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Barden,N., Sillaber,I. and Paez-Pereda,M.
TITLE Means and methods for diagnosing and treating affective disorders
JOURNAL Patent: WO 2004092384-A 56 28-OCT-2004;
NeuroNova Aktiengesellschaft (DE)
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RESULT 23
CQ897253/c
LOCUS CQ897253 23 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 56 from Patent WO2004092384.
ACCESSION CQ897253
VERSION CQ897253.1 GI:55582073
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Barden,N., Sillaber,I. and Paez-Pereda,M.
TITLE Means and methods for diagnosing and treating affective disorders
JOURNAL Patent: WO 2004092384-A 56 28-OCT-2004;
NeuroNova Aktiengesellschaft (DE)
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LOCUS CQ890713 23 bp DNA linear PAT 01-NOV-2004
DEFINITION Sequence 56 from Patent EP1469072.
ACCESSION CQ890713
VERSION CQ890713.1 GI:55163634
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Barden,N., Sillaber,I. and Paez-Pereda,M.
TITLE Means and methods for diagnosing and treating affective disorders
JOURNAL Patent: EP 1469072-A 56 20-OCT-2004;
NeuroNova Aktiengesellschaft (DE)
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QY 2 ATCAAAGGTGGCGGAG 17
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Db 4 ATCAAAGGGGGACGAG 19
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LOCUS CQ890713 23 bp DNA linear PAT 01-NOV-2004
DEFINITION Sequence 56 from Patent EP1469072.
ACCESSION CQ890713
VERSION CQ890713.1 GI:55163634
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Barden,N., Sillaber,I. and Paez-Pereda,M.
TITLE Means and methods for diagnosing and treating affective disorders
JOURNAL Patent: EP 1469072-A 56 20-OCT-2004;
NeuroNova Aktiengesellschaft (DE)
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 4 ATCAAAGGGGGACGAG 19
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 2 ATCAAGGTGGCCGAG 17  
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 LOCUS CQ898402 23 bp DNA linear PAT 08-NOV-2004  
 DEFINITION Sequence 56 from Patent EP1473367.  
 ACCESSION CQ898402  
 VERSION CQ898402.1 GI:55582721  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1  
 Barden, N., Sillaber, I. and Paez-Pereda, M.  
 Means and methods for diagnosing and treating affective disorders  
 Patent: EP 1473367-A 56 03-NOV-2004;  
 NeuroNova Aktiengesellschaft (DE)

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 Db 16 ATCAAGCTGGACGAG 1

RESULT 25  
 AX206899/c  
 LOCUS AX206899 27 bp DNA linear PAT 30-AUG-2001  
 DEFINITION Sequence 7 from Patent WO0155429.  
 ACCESSION AX206899  
 VERSION AX206899.1 GI:15394711  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 Mattanovich, D., Katinger, H., Hohenblum, H., Naschberger, S. and  
 Weisk, R.  
 Method for the manufacture of recombinant trypsin  
 Patent: WO 0155429-A 7 02-AUG-2001;  
 Polymun Scientific Immunobiologische Forschung GmbH (AT)

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ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 27;  
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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Perfect score: 18  
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Post-processing: Minimum Match 0%  
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- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	13.8	76.7	47	AAQ63832	Aaq63832 Oligonuc
5	13.4	74.4	39	ADM94051	Adm94051 Rearrange
6	13.4	74.4	44	AAAD11004	Aad11004 Human try
7	13.4	74.4	45	AAAD09077	Aad09077 Human oli
8	13.4	74.4	63	ABZ76323	Abz76323 Plasmid p
9	13.4	74.4	65	ABN29541	Abn29541 Rat splic
10	13.2	73.3	22	ABE79786	Aeb79786 Drosophil
11	13.2	73.3	22	ABE79480	Aeb79480 Drosophil
12	13.2	73.3	22	ABE79324	Aeb79324 Caenorhab
13	13.2	73.3	22	ABE79630	Aeb79630 Caenorhab
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16	13.2	73.3	23	ADW06866	Adw06866 siRNA ant
17	13.2	73.3	23	ADY31025	Ady31025 Micro RNA
18	13.2	73.3	23	ADY31024	Ady31024 Micro RNA
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22	13.2	73.3	72	9	ADA37054	Ada37054 Sim-2-CTL
23	13.2	73.3	76	13	ACF04460	Acf04460 Biomolecu
24	13.2	73.3	76	13	ADR83553	Adr83553 Human DNA
25	13	72.2	18	2	AAQ27315	Aaq27315 PCR prime
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27	13	72.2	18	2	AAQ96135	Aaq96135 Human C-b
28	13	72.2	18	2	AAV64293	Aav64293 Human T c
29	13	72.2	18	4	AAF85281	Aaf85281 PCR prime
30	13	72.2	18	5	AAF27154	Aaf27154 Human TCR
31	12.8	71.1	17	8	ACC67899	Acc67899 Murine ol
32	12.8	71.1	17	8	ACC67899	Acc67899 Murine ol
33	12.8	71.1	20	3	AAF22198	Aaf22198 Arabidops
34	12.8	71.1	20	6	ABL94449	Ab194449 Mouse C/E
35	12.8	71.1	21	13	ADU31111	Adu31111 Knock-dow
36	12.8	71.1	23	13	ADT25987	Adt25987 P2X7R ion
37	12.8	71.1	23	13	ADU23814	Adu23814 Human ATP
38	12.8	71.1	25	9	ACI14729	Act14729 Human mic
39	12.8	71.1	26	14	ADM75569	Adm75569 Epstein B
40	12.8	71.1	26	5	AA522050	Aas22050 Human COL
41	12.8	71.1	27	4	AAAD11009	Aad11009 Human try
42	12.8	71.1	29	3	AAZ33403	Aaz33403 Human try
43	12.8	71.1	37	2	AAT36734	Aat36734 Rat vasop
44	12.8	71.1	38	2	AAQ63831	Aaq63831 Oligonuc
45	12.8	71.1	42	14	ABE11187	Aeb11187 Mutagenes
46	12.8	71.1	52	2	AAQ31788	Aaq31788 Primer KS
47	12.8	71.1	57	14	ADY21518	Ady21518 Anti-CD37
48	12.8	71.1	60	6	ABN50725	Abn50725 Human spl
49	12.8	71.1	60	14	ADY21591	Ady21591 Antibody
50	12.8	71.1	60	14	ADY21589	Ady21589 Antibody
51	12.8	71.1	65	6	ABN51818	Abn51818 Mouse spl
52	12.8	71.1	65	6	ABN27922	Abn27922 Rat splic
53	12.8	71.1	65	6	ABN53195	Abn53195 Mouse spl
54	12.8	71.1	65	6	ABN31403	Abn31403 Rat splic
55	12.8	71.1	74	14	ABE50316	Aeb50316 Human cal
56	12.8	68.9	75	14	AA54972	Aas4972 m22(tscFv)
57	12.4	68.9	18	4	AA513755	Aas13755 Simple se
58	12.4	68.9	19	5	AAH83288	Aah83288 cdk8 ribo
59	12.4	68.9	19	5	AAH58450	Aah58450 Cell-cycl
60	12.4	68.9	20	6	ADP39686	Adp39686 Human GPx
61	12.4	68.9	20	6	ABL50080	Ab150080 Detergent
62	12.4	68.9	20	10	ABZ87053	Abz87053 Human oli
63	12.4	68.9	20	11	ABD23283	Abd23283 Human myo
64	12.4	68.9	24	3	AAAC87764	Aac87764 SNORF36 r
65	12.4	68.9	24	3	AAAC87788	Aac87788 Human SNO
66	12.4	68.9	24	4	AAAF76353	Aaf76353 Human kIo
67	12.4	68.9	26	12	ADP12202	Adp12202 Taqman pr
68	12.4	68.9	29	3	AAA23981	Aaa23981 Oestrogen
69	12.4	68.9	32	4	AAD11008	Aad11008 Human try
70	12.4	68.9	33	12	ADK60398	Adk60398 Angiogene
71	12.4	68.9	33	12	ADK60699	Adk60699 Angiogene
72	12.4	68.9	37	3	AAA50913	Aaa50913 Human CD4
73	12.4	68.9	40	14	ADM78469	Adm78469 Hybridiz
74	12.4	68.9	45	3	AAAC87758	Aac87758 SNORF36 r
75	12.4	68.9	50	2	AAQ93217	Aaq93217 Primer CS
76	12.4	68.9	50	6	ABZ04067	Abz04067 Human leu
77	12.4	68.9	51	4	AAI26947	Aai26947 Human SNP
78	12.4	68.9	51	4	AAI31431	Aai31431 Human SNP
79	12.4	68.9	60	6	ABN34848	Abn34848 Human SNP
80	12.4	68.9	77	14	ADW26288	Adw26288 EGFR inh
81	12.2	67.8	20	3	AAZ58240	Aaz58240 Mouse gly
82	12.2	67.8	20	3	AAZ58240	Aaz58240 Mouse gly
83	12.2	67.8	20	6	AAZ58240	Aaz58240 Mouse gly
84	12.2	67.8	20	6	ABU57690	Abu57690 Human Gap
85	12.2	67.8	20	8	ABK15349	Abk15349 Glyceral
86	12.2	67.8	20	10	ABZ74935	Abz74935 Mouse acy
87	12.2	67.8	20	10	ABZ97862	Abz97862 Human sot
88	12.2	67.8	20	11	ABV75849	Abv75849 Human gly
89	12.2	67.8	20	11	ABD30893	Abd30893 Human sot
90	12.2	67.8	20	12	ADK94860	Adk94860 Primer of
91	12.2	67.8	20	12	ADJ59737	Adj59737 Oligonuc
92	12.2	67.8	20	12	ADO45227	Ado45227 Human oli
93	12.2	67.8	20	13	ADS00468	Ads00468 Human GAD

93 12.2 67.8 20 14 ADZ80653 PCR prime  
94 12.2 67.8 20 14 ADZ71209 Human GAP  
95 12.2 67.8 20 14 AEB22289  
c 96 12.2 67.8 21 6 ABA03932  
c 97 12.2 67.8 21 10 ADJ95309 Novel NOV  
c 98 12.2 67.8 21 12 ADL65387  
c 99 12.2 67.8 21 12 ADL27554 PCR prime  
c 100 12.2 67.8 22 6 ABK15251 Corn nk60

## ALIGNMENTS

RESULT 1  
AAH47975  
ID AAH47975 standard; DNA; 18 BP.  
XX AC  
XX AAH47975;  
XX AC  
XX 02-OCT-2001 (first entry)  
XX Human inducible NOS antisense oligonucleotide SEQ ID NO 19.  
XX  
XX Antisense oligonucleotide; inducible nitric oxide synthase; NOS;  
XX modulate expression; immunomodulator; antidiabetic; cardiovascular;  
XX cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
XX 2'-O-methoxyethyl; phosphorothioate; human; ss.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1..18  
XX /\*tag= a  
XX /mod\_base= OTHER  
XX /note= "phosphorothioate backbone, 5' and 3' four  
XX nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine  
XX residues in the 2'-MOE wings are 5-methylcytidines) and a  
XX deoxy gap"

WO200152902-A1.

26-JUL-2001.

15-JAN-2001; 2001WO-US001381.

24-JAN-2000; 2000US-00490208.

(ISIS-) ISIS PHARM INC.

Bennett CF, Dean NM, Cowse LM;

WPI; 2001-465340/50.

New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or ischemia.

Claim 3; Page 83; 144pp; English.

The invention relates to antisense compounds, especially oligonucleotides, which are targeted to a nucleic acid encoding inducible nitric oxide synthase and which specifically hybridize to and modulate expression of inducible nitric oxide synthase. The antisense compounds have immunomodulator, antidiabetic, cardiovascular, cardiac, neuroprotective, disorder and vasotropic activity. The antisense oligonucleotides are useful for inhibiting the expression of inducible nitric oxide synthase in cells or tissues. In particular, the antisense oligonucleotides are useful for treating diseases or disorders associated with inducible nitric oxide synthase, e.g. diabetes, immunological disorder, cardiovascular disorder, neurological disorder or ischemia/reperfusion injury. The antisense oligonucleotides are also useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a  
CC phosphorothioate backbone, a central "gap" region of ten nucleotides  
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine  
CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human  
CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)  
XX  
SQ Sequence 18 BP; 6 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18

Db 1 CATCAAGGTGGCCGAGA 18

## RESULT 2

ADF16779

ID ADF16779 standard; DNA; 36 BP.

XX AC

XX ADF16779;

XX 12-FEB-2004 (first entry)

XX Human albumin fusion protein-related PCR primer SeqID1957.  
XX  
XX albumin fusion protein; albumin activity; human serum albumin;  
XX serum osmotic pressure; shelf-life; stability; antidiabetic;  
XX gene therapy; diabetes mellitus; human; PCR; primer; ss.

XX Homo sapiens.

XX WO2003060071-A2.

XX 24-JUL-2003.

XX 23-DEC-2002; 2002WO-US040891.

XX 21-DEC-2001; 2001US-0341811P.

XX 24-JAN-2002; 2002US-0350358P.

XX 28-JAN-2002; 2002US-0351360P.

XX 26-FEB-2002; 2002US-0359370P.

XX 28-FEB-2002; 2002US-0360000P.

XX 08-APR-2002; 2002US-0370227P.

XX 10-MAY-2002; 2002US-0378950P.

XX 24-MAY-2002; 2002US-0382617P.

XX 28-MAY-2002; 2002US-0383123P.

XX 05-JUN-2002; 2002US-0385708P.

XX 10-JUL-2002; 2002US-0394625P.

XX 24-JUL-2002; 2002US-0398008P.

XX 09-AUG-2002; 2002US-0402131P.

XX 13-AUG-2002; 2002US-0402708P.

XX 18-SEP-2002; 2002US-0411355P.

XX 18-SEP-2002; 2002US-0411426P.

XX 02-OCT-2002; 2002US-0414984P.

XX 11-OCT-2002; 2002US-0417611P.

XX 23-OCT-2002; 2002US-0420246P.

XX 05-NOV-2002; 2002US-0423623P.

XX (HUMA-) HUMAN GENOME SCI INC.  
XX (DELZ-) DELTA BIOTECHNOLOGY LTD.  
XX (PRIN-) PRINCIPIA PHARM CORP.

PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;

XX WPI; 2003-598517/56.

XX New albumin fusion protein, useful for preparing a composition for  
XX treating diabetes mellitus.

XX Example 4; SEQ ID NO 1957; 24pp; English.

XX This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also  
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of  
 CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production of compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a PCR primer which may  
 CC be used for amplification of a DNA sequence encoding a therapeutic  
 CC protein which was fused with human albumin to create a novel albumin  
 CC fusion protein of the invention. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 36 BP; 8 A; 8 C; 13 G; 7 T; 0 U; 0 Other;  
 Query Match 76.7%; Score 13.8; DB 10; Length 36;  
 Best Local Similarity 88.2%; Pred. No. 2.3e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 ATCAAGGTGGCCGAGA 18  
 Db |||||  
 15 ATCAAGGTGGCGTAGA 31  
 RESULT 3  
 ADF16777  
 ID ADF16777 standard; DNA; 36 BP.  
 AC ADF16777;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human albumin fusion protein-related PCR primer SeqID1955.  
 XX  
 KW albumin fusion protein; albumin activity; human serum albumin;  
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;  
 KW gene therapy; diabetes mellitus; human; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003060071-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PF 23-DEC-2002; 2002WO-US040891.  
 XX  
 PR 21-DEC-2001; 2001US-0341811P.  
 PR 24-JAN-2002; 2002US-0350358P.  
 PR 28-JAN-2002; 2002US-0351360P.  
 PR 26-FEB-2002; 2002US-0359370P.  
 PR 28-FEB-2002; 2002US-0360000P.  
 PR 27-MAR-2002; 2002US-0367500P.  
 PR 08-APR-2002; 2002US-0370227P.  
 PR 10-MAY-2002; 2002US-0378950P.  
 PR 24-MAY-2002; 2002US-0382617P.  
 PR 28-MAY-2002; 2002US-0383123P.  
 PR 05-JUN-2002; 2002US-0385708P.  
 PR 10-JUL-2002; 2002US-0394625P.  
 PR 24-JUL-2002; 2002US-0398008P.  
 PR 09-AUG-2002; 2002US-0402131P.  
 PR 13-AUG-2002; 2002US-0402708P.  
 PR 18-SEP-2002; 2002US-0411355P.  
 PR 18-SEP-2002; 2002US-0411426P.  
 PR 02-OCT-2002; 2002US-0414984P.  
 PR 11-OCT-2002; 2002US-0417611P.  
 PR 23-OCT-2002; 2002US-0420246P.  
 PR 05-NOV-2002; 2002US-0423623P.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
 PA (PRIN-) PRINCIPIA PHARM CORP.  
 XX  
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;  
 XX WPI; 2003-598517/56.  
 DR  
 XX New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.  
 XX  
 PS Example 4; SEQ ID NO 1955; 24pp; English.  
 XX  
 CC This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also  
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of  
 CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production of compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a PCR primer which may  
 CC be used for amplification of a DNA sequence encoding a therapeutic  
 CC protein which was fused with human albumin to create a novel albumin  
 CC fusion protein of the invention. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 36 BP; 8 A; 8 C; 13 G; 7 T; 0 U; 0 Other;  
 Query Match 76.7%; Score 13.8; DB 10; Length 36;  
 Best Local Similarity 88.2%; Pred. No. 2.3e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 ATCAAGGTGGCCGAGA 18  
 Db |||||  
 15 ATCAAGGTGGCGTAGA 31  
 RESULT 4  
 AAQ63832/c  
 ID AAQ63832 standard; DNA; 47 BP.  
 XX  
 AC AAQ63832;  
 XX  
 DT 07-FEB-1995 (first entry)  
 XX  
 DE Oligonucleotide IKGR, used in construction of modified t-PA.  
 XX  
 KW Tissue plasminogen activator; t-PA; modified; variant;  
 KW plasmin cleavage recognition site; C-terminal peptide; systemic bleeding;  
 KW decrease; reduce; thrombosis treatment; anti-thrombotic; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06133780-A.  
 XX  
 PD 17-MAY-1994.  
 XX  
 PF 23-OCT-1992; 92JP-00309285.  
 XX  
 PR 23-OCT-1992; 92JP-00309285.  
 XX  
 PA (SUMU) SUMITOMO SEIYAKU KK.  
 XX  
 DR WPI; 1994-196164/24.  
 XX  
 PT New modified tissue plasminogen activator - comprises sequence which is  
 PT recognised and cleaved by plasmin.  
 XX  
 PS Example 2; Page 8; 10pp; Japanese.

XX Oligonucleotide pairs DC and DCR, DO and DOR, and IKGG and IKGR (see  
 CC AAQ63827-063832) are annealed to produce 3 double-stranded fragments. The  
 CC fragments are ligated together to produce a fragment which can be  
 CC amplified by the polymerase chain reaction using oligonucleotides DC and  
 CC IKGR as primers. The amplified fragment was digested with BstEII and  
 CC SalI and the resulting fragment was used in the construction of plasmid  
 CC pUC-D01. The plasmid codes for a modified t-PA with a plasmin cleavage  
 CC site at its C-terminal end  
 XX Sequence 47 BP; 8 A; 13 C; 12 G; 14 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 2; Length 47;  
 Best Local Similarity 88.2%; Pred. No. 2.4e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17  
 |||||  
 Db 39 CATCAAGGAGCCCTAG 23

## RESULT 5

ADM94051/c  
 ID ADM94051 standard; DNA; 39 BP.

XX AC ADM94051;

XX DT 15-JUL-2004 (first entry)

XX DE Rearranged Ig and TCR gene related nucleotide.

XX KW nucleic acid amplification; primer; PCR; detection;

XX KW chromosomal translocation; human; clonal rearrangement;

XX KW chromosome aberration; lymphoproliferative disorder; Ig; TCR; gene; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004033728-A2.

XX PD 22-APR-2004.

XX PF 13-OCT-2003; 2003WO-NL000690.

XX PR 11-OCT-2002; 2002US-0417779P.

XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PA (DAVI/) DAVI F B L.

XX PI Van Dongen JJM, Langerak AW, Schuurink EMD, San Miquel JF;

XX PI Garzia Sanz R, Parreira A, Smith JL, Lavender FL, Morgan GJ;

XX PI Evans PAS, Kneba M, Hummel M, Macintyre EA, Bastard C;

XX DR WPI; 2004-364878/34.

XX PT New set of nucleic amplification primers comprising a forward primer and  
 PT a reverse primer and capable of amplifying a rearrangement, useful in  
 PT diagnosing lymphoproliferative disorders.

XX PS Disclosure; Fig 2; 121pp; English.

XX The present invention describes a set of nucleic amplification primers  
 CC capable of amplifying a VH-JH or DH-JH IGH, VK-JK or VK/intron-Kde IGH,  
 CC Vlambda-Jlambda IGL, Vbeta-Jbeta TCRB or Dbeta-Jbeta TCRB, VI-JY TCRG,  
 CC Vdelta-Jdelta, Ddelta-Ddelta or Vdelta-Ddelta TCRD rearrangement  
 CC comprises a forward primer and a reverse primer. Also described: (1) a  
 CC nucleic acid amplification assay, preferably a PCR or multiplex PCR  
 CC assay, using the set of primers; (2) detecting VH-JH or DH-JH IGH, VK-JK  
 CC or VK/intron-Kde IGH, Vlambda-Jlambda IGL, Vbeta-Jbeta TCRB or Dbeta-  
 CC Jbeta TCRB, VI-JY TCRG, Vdelta-Jdelta, Ddelta-Ddelta or Vdelta-Ddelta  
 CC TCRD rearrangement; (3) detecting chromosomal translocation (11;14)(BCLg-  
 CC JG2-1) or t(14;18)(BCL2-IGH); (4) detecting human TBXAS1, recombination  
 CC activating protein (RAG1), promyelocytic leukaemia zinc finger protein

CC (PLZF) or AP4 gene; (5) assessing clonal rearrangements and/or chromosome  
 CC aberrations; and (6) a kit for the detecting at least one rearrangement  
 CC comprising the set of primers. The new set of nucleic amplification  
 CC primers capable of amplifying a VH-JH or DH-JH IGH, VK-JK or VK/intron-  
 CC Kde IGH, Vlambda-Jlambda IGL, Vbeta-Jbeta TCRB or Dbeta-Jbeta TCRB, VI-JY  
 CC TCRG, Vdelta-Jdelta, Ddelta-Ddelta or Vdelta-Ddelta TCRD rearrangement  
 CC are useful in diagnosing lymphoproliferative disorders. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX Sequence 39 BP; 7 A; 13 C; 11 G; 8 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 12; Length 39;  
 Best Local Similarity 93.3%; Pred. No. 3.8e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCAAGGTGGCCGAG 17  
 |||||  
 Db 32 TCAAGGGGGCCGAG 18

## RESULT 6

AAD11004/c

ID AAD11004 standard; DNA; 44 BP.

XX AC AAD11004;

XX DT 24-SEP-2001 (first entry)

XX DE Human trypsinogen 1 gene cloning forward PCR primer #1.

XX KW Human; trypsinogen 1; trypsin; protein refolding; inclusion body;

XX KW pPICZalphaB plasmid; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200155429-A2.

XX PD 02-AUG-2001.

XX PF 24-JAN-2001; 2001WO-EP000770.

XX PR 24-JAN-2000; 2000US-0177348P.

XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX PI Mattanovich D, Katinger H, Hohenblum H, Naschberger S, Weik R;

XX DR WPI; 2001-457733/49.

XX PT Recombinant manufacture of trypsin, comprises transforming a host cell,  
 PT incubating the transformed cells, and separating and optionally  
 PT processing the trypsinogen.

XX PS Example 1; Page 9; 22pp; English.

XX The invention relates to a method for the manufacture and purification of  
 CC recombinant trypsinogen and trypsin in E. coli and yeast, using high  
 CC yield expression vectors with and without secretion leader sequences. The  
 CC invention also relates to an improved method and apparatus for carrying  
 CC out protein refolding specifically useful for processing trypsinogen that  
 CC has accumulated intracellularly in the form of inclusion bodies. The  
 CC present DNA sequence is a forward PCR primer which is used for cloning  
 CC human trypsinogen 1 gene into the pPICZalphaB plasmid. The PCR primer is  
 CC also used for expressing human trypsinogen 1 in the yeast Pichia pastoris  
 XX Sequence 44 BP; 7 A; 16 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 4; Length 44;  
 Best Local Similarity 93.3%; Pred. No. 3.9e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCG 15  
 |||||

Db 38 CATCAAGGGGCGC 24

RESULT 7  
AAD09077  
XX AAD09077 standard; DNA; 45 BP.  
XX  
AC AAD09077;  
XX  
XX 04-SEP-2001 (first entry)  
XX  
DE Human oligonucleotide HOG-799 used to construct pMWC22.  
XX  
KW Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;  
KW cytoskeletal; therapy; Alzheimer's disease; Parkinson's disease; injury;  
KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;  
KW nervous system aging; neurodegenerative disease; immunological disease;  
KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;  
KW extracellular signalling protein; HOG-799; ss.  
XX  
OS Homo sapiens.  
XX  
XX W0200134654-A1.  
XX  
PD 17-MAY-2001.  
XX  
XX 02-NOV-2000; 2000WO-US030405.  
XX  
PF 05-NOV-1999; 99US-0164025P.  
XX  
PR (BIOJ ) BIOGEN INC.  
XX  
PA Strauch K;  
XX  
XX PI  
XX  
XX WPI; 2001-329075/34.  
XX  
DR Novel isolated hedgehog fusion polypeptide useful for treating  
XX neurological conditions such as Alzheimer's disease, Parkinson's disease,  
PT Huntington's chorea, amyotrophic lateral sclerosis, and multiple  
PT sclerosis.  
XX  
PS Example 1; Page 62; 178pp; English.  
XX  
CC The present invention relates to hedgehog fusion proteins. Hedgehog  
CC proteins are a family of extracellular signalling proteins that regulate  
CC various aspects of embryonic development both in vertebrates and in  
CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or  
CC treatment of any condition or disease state for which a hedgehog or  
CC patched protein constituent is efficacious and in the diagnosis of  
CC constituents or conditions of disease states in biological systems or  
CC specimens and for diagnostic purposes in non-physiological systems.  
CC Hedgehog fusion protein is useful for treating neurological conditions  
CC due to injury, aging of nervous system, including Alzheimer's disease,  
CC chronic neurodegenerative diseases of the nervous system, including  
CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis  
CC and chronic immunological diseases of nervous system including multiple  
CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal  
CC tumours and to specifically target medical therapies against cancers and  
CC tumours which express the receptor for the protein. The present sequence  
CC is human oligonucleotide HOG-799 used to construct pMWC22, pMWC23, pMWC25  
CC and pMWC26 plasmids which are used in the invention  
XX  
SQ Sequence 45 BP; 12 A; 14 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 4; Length 45;  
Best Local Similarity 93.3%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 4 CAAGGTGGCCGAGA 18  
| | | | | | | | | |  
DB 26 CCAGGTGGCCGAGA 40

XX	RESULT 8	
XX	ABZ76323/c	
XX	ID ABZ76323 standard; DNA; 63 BP.	
XX	AC ABZ76323;	
XX	DT 12-JUN-2003 (first entry)	
XX	Plasmid pIGT3 constructing antisense primer P4.	
XX	Helper phage; Ex-phage; phagemid vector; coat protein; mutant;	
XX	phage display; PCR; primer; ss.	
XX	Synthetic.	
XX	WO2003018785-A1.	
XX	PN 06-MAR-2003.	
XX	PD 28-MAY-2002; 2002WO-KR001001.	
XX	PF 29-AUG-2001; 2001KR-00052451.	
XX	PR (IGTH-) IG THERAPY CO LTD.	
XX	PA Cha S;	
XX	PI WPI; 2003-300730/29.	
XX	DR New mutant helper phage, termed Ex-phage, useful for packaging a phagemid	
XX	PT vector, isolating antibody molecules in phage display, or probing	
XX	PT candidate molecules for the development of therapeutic antibody drugs.	
XX	PS Example 2; Page 50; 54pp; English.	
XX	CC The invention relates to a mutant helper phage, termed Ex-phage, for	
XX	CC packaging a phagemid vector containing filamentous virus genome of which	
XX	CC at least a part of the gene of wild-type minor coat protein is deleted or	
XX	CC defective. Conditional suppressive translation stop codon is introduced	
XX	CC at the N-terminal of the gene of minor coat protein of the mutant helper	
XX	CC phage. The mutant helper phage is useful for packaging a phagemid vector,	
XX	CC isolating an antibody and selecting a recombinant virus expressing	
XX	CC antibodies. The method is useful for isolating antibody molecules in	
XX	CC phage display, or increasing display level of foreign polypeptides on the	
XX	CC surface of recombinant phage in phage display technology. The phage	
XX	CC display library can be used at probing candidate molecules for the	
XX	CC development of therapeutic antibody drugs. Sequences ABZ76322-324	
XX	CC represent PCR primers used in the construction of a plasmid pIGT3	
XX	SQ Sequence 63 BP; 6 A; 18 C; 14 G; 25 T; 0 U; 0 Other;	
	Query Match 74.4%; Score 13.4; DB 8; Length 63;	
	Best Local Similarity 93.3%; Pred. No. 4.1e+03;	
	Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2 ATCAAGCTGGCCGA 16	
DB	48 ATCAAGCTGGCCGA 34	
XX	RESULT 9	
XX	ABN29541	
XX	ID ABN29541 standard; DNA; 65 BP.	
XX	AC ABN29541;	
XX	DT 15-JUL-2002 (first entry)	
XX	Rat spliced transcript detection oligonucleotide SEQ ID NO:2289.	
XX	Human; mouse; rat; splice transcript; detection; RNA transcript;	
XX	splice variant; transcriptome; oligonucleotide library; ss.	

OS Rattus norvegicus.  
 PN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 XX 20-JUL-2001; 2001WO-IB001903.  
 XX  
 XX 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 XX (COMP-) COMPUGEN INC.  
 XX  
 XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 PI WPI; 2002-257383/30.  
 XX  
 XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 XX Example 1; SEQ ID NO 2289; 47pp; English.  
 PS  
 XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 65 BP; 16 A; 15 C; 18 G; 16 T; 0 U; 0 Other;  
 Query Match 74.4%; Score 13.4; DB 6; Length 65;  
 Best Local Similarity 93.3%; Pred. No. 4.1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 CAAGAAGTGGCCGAGA 18  
 DB 2 CAAGAAGTGGCCGAGA 16  
 RESULT 10  
 AEB79786  
 ID AEB79786 standard; RNA; 22 BP.  
 XX  
 AC AEB79786;  
 XX  
 XX 20-OCT-2005 (first entry)  
 DT  
 XX Drosophila melanogaster dme-miR-2c-targeted anti-microRNA, SEQ:610.  
 DE  
 XX RNA interference; gene silencing; anti-microRNA; anti-miRNA;  
 KW microRNA inhibitor; miRNA inhibitor; gene expression; gene regulation;  
 XX ss.  
 XX

OS Drosophila melanogaster.  
 XX  
 PN US2005182005-A1.  
 XX  
 PD 18-AUG-2005.  
 XX  
 XX 13-MAY-2004; 2004US-00845057.  
 XX  
 XX 13-FEB-2004; 2004US-00778908.  
 PR  
 XX (TUSC/) TUSCHL T H.  
 PA (LAND/) LANDTHALER M.  
 PA (WEIS/) MEISTER G.  
 PA (PFEF/) PFEFFER S.  
 XX  
 XX Tuschl TH, Landthaler M, Meister G, Pfeiffer S;  
 PI WPI; 2005-554283/56.  
 XX  
 XX New isolated single stranded anti-microRNA molecule comprising a minimum  
 PT of ten moieties and a maximum of fifty moieties on a molecular backbone,  
 PT useful for inhibiting micro ribonucleoprotein particle (microRNP)  
 PT activity in a cell.  
 XX  
 XX Claim 1; SEQ ID NO 610; 115pp; English.  
 PS  
 XX The invention relates to isolated single-stranded anti-microRNA molecules  
 CC capable of inhibiting microRNP (microribonucleoprotein) activity. The  
 CC anti-microRNAs are: a) 10-50 bases in length; b) comprise unmodified or  
 CC modified ribonucleotides; c) comprise a region of at least 10 contiguous  
 CC bases identical to a portion of one of the human, mouse, rat, Drosophila  
 CC or Caenorhabditis elegans anti-microRNAs shown in AEB79483-AEB79788,  
 CC except that up to 30% of the bases are wobble bases, up to 10% of the  
 CC contiguous bases may be insertions, deletions, mismatches or combinations  
 CC thereof, and no more than 50% of these contiguous bases have  
 CC deoxyribonucleotide backbones; and d) have a mismatch with the base at  
 CC position 11 of the target microRNA. The invention also relates to a  
 CC method of inhibiting microRNP activity in a cell using the anti-microRNAs  
 CC of the invention, especially a human, mouse, rat, Drosophila or  
 CC Caenorhabditis elegans anti-microRNA. The invention further relates to  
 CC isolated microRNA molecules modified for increased nuclease resistance  
 CC which are: i) 10-50 bases in length; and ii) comprise at least 10  
 CC contiguous bases identical to one of the human, mouse, rat, Drosophila or  
 CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-  
 CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%  
 CC of the contiguous bases may be insertions, deletions, mismatches or  
 CC combinations thereof, and no more than 50% of these contiguous bases have  
 CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an  
 CC inserted or deleted base or a base substitution at position 11. The anti-  
 CC microRNAs and microRNAs of the invention are useful for modulating gene  
 CC expression. As a component of animal microRNPs, microRNAs guide RNA  
 CC degradation in a similar way to short interfering RNA (siRNA)-induced  
 CC silencing complexes. Such microRNAs may be beneficial or harmful to cell  
 CC survival. If a particular microRNA is known to be beneficial, an  
 CC appropriate isolated microRNA of the invention may be introduced into a  
 CC cell to promote survival. Conversely, if a particular microRNA is known  
 CC to be harmful (e.g., one known to induce apoptosis or induce cancer),  
 CC then an appropriate anti-microRNA of the invention can be introduced into  
 CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or  
 CC microRNAs of the invention may be introduced into a cell to study the  
 CC function of the microRNA. Sequences AEB79733-AEB79788 represent  
 CC specifically claimed Drosophila microRNA-directed anti-microRNAs upon  
 CC which anti-microRNAs of the invention may be based.  
 XX  
 SQ Sequence 22 BP; 6 A; 6 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 73.3%; Score 13.2; DB 14; Length 22;  
 Best Local Similarity 72.2%; Pred. No. 4.6e+03;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CATCAAGGTGGCCGAGA 18  
 DB 3 CAUCAAAGTGGCUGUGA 20



RESULT 11  
AEB79480/c  
ID AEB79480 standard; RNA; 22 BP.  
XX AC AEB79480;  
XX AC  
XX DT 20-OCT-2005 (first entry)  
XX DE Drosophila melanogaster microRNA dme-miR-2c, SEQ:304.  
XX DE  
XX KW RNA interference; gene silencing; microRNA; miRNA; gene expression;  
XX KW gene regulation; ss.  
XX OS Drosophila melanogaster.  
XX XX  
XX PN US2005182005-A1.  
XX PD 18-AUG-2005.  
XX PF 13-MAY-2004; 2004US-00845057.  
XX PR 13-FEB-2004; 2004US-00778908.  
XX PA (TUSC/) TUSCHL T H.  
XX PA (LAND/) LANDTHALER M.  
XX PA (MEIS/) MEISTER G.  
XX PA (PFEF/) PFEFFER S.  
XX PI Tuschl TH, Landthaler M, Meister G, Pfeffer S;  
XX DR WPI; 2005-554283/56.  
XX XX  
XX PT New isolated single stranded anti-microRNA molecule comprising a minimum  
XX PT of ten moieties and a maximum of fifty moieties on a molecular backbone,  
XX PT useful for inhibiting micro ribonucleoprotein particle (microRNP)  
XX PT activity in a cell.  
XX PS Claim 45; SEQ ID NO 304; 115pp; English.  
XX CC The invention relates to isolated single-stranded anti-microRNA molecules  
XX CC capable of inhibiting microRNP (microribonucleoprotein) activity. The  
XX CC anti-microRNAs are: a) 10-50 bases in length; b) comprise unmodified or  
XX CC modified ribonucleotides; c) comprise a region of at least 10 contiguous  
XX CC bases identical to a portion of one of the human, mouse, rat, Drosophila  
XX CC or Caenorhabditis elegans anti-microRNAs shown in AEB79483-AEB79788,  
XX CC except that up to 30% of the bases are wobble bases, up to 10% of the  
XX CC contiguous bases may be insertions, deletions, mismatches or combinations  
XX CC thereof, and no more than 50% of these contiguous bases have  
XX CC deoxyribonucleotide backbones; and d) have a mismatch with the base at  
XX CC position 11 of the target microRNA. The invention also relates to a  
XX CC method of inhibiting microRNP activity in a cell using the anti-microRNAs  
XX CC of the invention, especially a human, mouse, rat, Drosophila or  
XX CC Caenorhabditis elegans anti-microRNA. The invention further relates to  
XX CC isolated microRNA molecules modified for increased nuclease resistance  
XX CC which are: i) 10-50 bases in length; and ii) comprise at least 10  
XX CC contiguous bases identical to one of the human, mouse, rat, Drosophila or  
XX CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-  
XX CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%  
XX CC of the contiguous bases may be insertions, deletions, mismatches or  
XX CC combinations thereof, and no more than 50% of these contiguous bases have  
XX CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an  
XX CC inserted or deleted base or a base substitution at position 11. The anti-  
XX CC microRNAs and microRNAs of the invention are useful for modulating gene  
XX CC expression. As a component of animal microRNAs, microRNAs guide RNA  
XX CC degradation in a similar way to short interfering RNA (siRNA)-induced  
XX CC silencing complexes. Such microRNAs may be beneficial or harmful to cell  
XX CC survival. If a particular microRNA is known to be beneficial, an  
XX CC appropriate isolated microRNA of the invention may be introduced into a  
XX CC cell to promote survival. Conversely, if a particular microRNA is known  
XX CC to be harmful (e.g., one known to induce apoptosis or induce cancer),  
XX CC then an appropriate anti-microRNA of the invention can be introduced into

CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or  
CC microRNAs of the invention may be introduced into a cell to study the  
CC function of the microRNA. Sequences AEB79426-AEB79482 represent  
CC specifically claimed Drosophila microRNAs upon which microRNAs of the  
CC invention may be based and which are targets for anti-microRNAs of the  
CC invention.  
XX SQ Sequence 22 BP; 5 A; 5 C; 6 G; 0 T; 6 U; 0 Other;  
XX  
XX Query Match 73.3%; Score 13.2; DB 14; Length 22;  
XX Best Local Similarity 83.3%; Pred. No. 4 6e+03;  
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 CATCAAAGTGGCCGAGA 18  
DB 20 CATCAAAGTGGCTGTGA 3  
RESULT 12  
AEB79324/c  
ID AEB79324 standard; RNA; 22 BP.  
XX AC AEB79324;  
XX DT 20-OCT-2005 (first entry)  
XX DE Caenorhabditis elegans microRNA Cel-miR-2, SEQ:148.  
XX DE  
XX KW RNA interference; gene silencing; microRNA; miRNA; gene expression;  
XX KW gene regulation; ss.  
XX OS Caenorhabditis elegans.  
XX PN US2005182005-A1.  
XX PD 18-AUG-2005.  
XX PF 13-MAY-2004; 2004US-00845057.  
XX PR 13-FEB-2004; 2004US-00778908.  
XX PA (TUSC/) TUSCHL T H.  
XX PA (LAND/) LANDTHALER M.  
XX PA (MEIS/) MEISTER G.  
XX PA (PFEF/) PFEFFER S.  
XX PI Tuschl TH, Landthaler M, Meister G, Pfeffer S;  
XX DR WPI; 2005-554283/56.  
XX XX  
XX PT New isolated single stranded anti-microRNA molecule comprising a minimum  
XX PT of ten moieties and a maximum of fifty moieties on a molecular backbone,  
XX PT useful for inhibiting micro ribonucleoprotein particle (microRNP)  
XX PT activity in a cell.  
XX PS Claim 45; SEQ ID NO 148; 115pp; English.  
XX CC The invention relates to isolated single-stranded anti-microRNA molecules  
XX CC capable of inhibiting microRNP (microribonucleoprotein) activity. The  
XX CC anti-microRNAs are: a) 10-50 bases in length; b) comprise unmodified or  
XX CC modified ribonucleotides; c) comprise a region of at least 10 contiguous  
XX CC bases identical to a portion of one of the human, mouse, rat, Drosophila  
XX CC or Caenorhabditis elegans anti-microRNAs shown in AEB79483-AEB79788,  
XX CC except that up to 30% of the bases are wobble bases, up to 10% of the  
XX CC contiguous bases may be insertions, deletions, mismatches or combinations  
XX CC thereof, and no more than 50% of these contiguous bases have  
XX CC deoxyribonucleotide backbones; and d) have a mismatch with the base at  
XX CC position 11 of the target microRNA. The invention also relates to a  
XX CC method of inhibiting microRNP activity in a cell using the anti-microRNAs  
XX CC of the invention, especially a human, mouse, rat, Drosophila or  
XX CC Caenorhabditis elegans anti-microRNA. The invention further relates to  
XX CC isolated microRNA molecules modified for increased nuclease resistance  
XX CC which are: i) 10-50 bases in length; and ii) comprise at least 10  
XX CC contiguous bases identical to one of the human, mouse, rat, Drosophila or  
XX CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-  
XX CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%  
XX CC of the contiguous bases may be insertions, deletions, mismatches or  
XX CC combinations thereof, and no more than 50% of these contiguous bases have  
XX CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an  
XX CC inserted or deleted base or a base substitution at position 11. The anti-  
XX CC microRNAs and microRNAs of the invention are useful for modulating gene  
XX CC expression. As a component of animal microRNAs, microRNAs guide RNA  
XX CC degradation in a similar way to short interfering RNA (siRNA)-induced  
XX CC silencing complexes. Such microRNAs may be beneficial or harmful to cell  
XX CC survival. If a particular microRNA is known to be beneficial, an  
XX CC appropriate isolated microRNA of the invention may be introduced into a  
XX CC cell to promote survival. Conversely, if a particular microRNA is known  
XX CC to be harmful (e.g., one known to induce apoptosis or induce cancer),  
XX CC then an appropriate anti-microRNA of the invention can be introduced into

CC contiguous bases identical to one of the human, mouse, rat, Drosophila or  
 CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-  
 CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%  
 CC of the contiguous bases may be insertions, deletions, mismatches or  
 CC combinations thereof, and no more than 50% of these contiguous bases have  
 CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an  
 CC inserted or deleted base or a base substitution at position 11. The anti-  
 CC microRNAs and microRNAs of the invention are useful for modulating gene  
 CC expression. As a component of animal microRNPs, microRNAs guide RNA  
 CC degradation in a similar way to short interfering RNA (siRNA)-induced  
 CC silencing complexes. Such microRNAs may be beneficial or harmful to cell  
 CC survival. If a particular microRNA is known to be beneficial, an  
 CC appropriate isolated microRNA of the invention may be introduced into a  
 CC cell to promote survival. Conversely, if a particular microRNA is known  
 CC to be harmful (e.g., one known to induce apoptosis or induce cancer),  
 CC then an appropriate anti-microRNA of the invention can be introduced into  
 CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or  
 CC microRNAs of the invention may be introduced into a cell to study the  
 CC function of the microRNA. Sequences AEB79321-AEB79426 represent  
 CC specifically claimed Caenorhabditis elegans microRNAs upon which  
 CC microRNAs of the invention may be based and which are targets for anti-  
 CC microRNAs of the invention.

XX SQ Sequence 22 BP; 5 A; 5 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 22;

Best Local Similarity 83.3%; Pred. No. 4.6e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18

||||||| :||| |||  
 Db 20 CATCAAGCTGGCTGTA 3

RESULT 13

AEB79630

ID AEB79630 standard; RNA; 22 BP.

AC AEB79630;

XX 20-OCT-2005 (first entry)

XX Caenorhabditis elegans Cel-miR-2-targeted anti-microRNA, SEQ:454.

XX RNA interference; gene silencing; anti-microRNA; anti-miRNA;

XX microRNA inhibitor; miRNA inhibitor; gene expression; gene regulation;

XX ss.

XX Caenorhabditis elegans.

XX US2005182005-A1.

XX 18-AUG-2005.

XX 13-MAY-2004; 2004US-00845057.

XX 13-FEB-2004; 2004US-00778908.

XX (TUSC/) TUSCHL T H.  
 XX (LAND/) LANDTHALER M.  
 XX (WEIS/) MEISTER G.  
 XX (PFEF/) PFEFFER S.

XX Tuschl TH, Landthaler M, Meister G, Pfeiffer S;

XX WPI; 2005-554283/56.

XX New isolated single stranded anti-microRNA molecule comprising a minimum  
 PT of ten moieties and a maximum of fifty moieties on a molecular backbone,  
 PT useful for inhibiting micro ribonucleoprotein particle (microRNP)  
 PT activity in a cell.

XX Claim 1; SEQ ID NO 454; 115pp; English.

XX The invention relates to isolated single-stranded anti-microRNA molecules  
 CC capable of inhibiting microRNP (microribonucleoprotein) activity. The  
 CC anti-microRNAs are: a) 10-50 bases in length; b) comprise unmodified or  
 CC modified ribonucleotides; c) comprise a region of at least 10 contiguous  
 CC bases identical to a portion of one of the human, mouse, rat, Drosophila  
 CC or Caenorhabditis elegans anti-microRNAs shown in AEB79483-AEB79788,  
 CC except that up to 30% of the bases are wobble bases, up to 10% of the  
 CC contiguous bases may be insertions, deletions, mismatches or combinations  
 CC thereof, and no more than 50% of these contiguous bases have  
 CC deoxyribonucleotide backbones; and d) have a mismatch with the base at  
 CC position 11 of the target microRNA. The invention also relates to a  
 CC method of inhibiting microRNP activity in a cell using the anti-microRNAs  
 CC of the invention, especially a human, mouse, rat, Drosophila or  
 CC Caenorhabditis elegans anti-microRNA. The invention further relates to  
 CC isolated microRNA molecules modified for increased nucleic acid resistance  
 CC which are: i) 10-50 bases in length; and ii) comprise at least 10  
 CC contiguous bases identical to one of the human, mouse, rat, Drosophila or  
 CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-  
 CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%  
 CC of the contiguous bases may be insertions, deletions, mismatches or  
 CC combinations thereof, and no more than 50% of these contiguous bases have  
 CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an  
 CC inserted or deleted base or a base substitution at position 11. The anti-  
 CC microRNAs and microRNAs of the invention are useful for modulating gene  
 CC expression. As a component of animal microRNPs, microRNAs guide RNA  
 CC degradation in a similar way to short interfering RNA (siRNA)-induced  
 CC silencing complexes. Such microRNAs may be beneficial or harmful to cell  
 CC survival. If a particular microRNA is known to be beneficial, an  
 CC appropriate isolated microRNA of the invention may be introduced into a  
 CC cell to promote survival. Conversely, if a particular microRNA is known  
 CC to be harmful (e.g., one known to induce apoptosis or induce cancer),  
 CC then an appropriate anti-microRNA of the invention can be introduced into  
 CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or  
 CC microRNAs of the invention may be introduced into a cell to study the  
 CC function of the microRNA. Sequences AEB79627-AEB79732 represent  
 CC specifically claimed Caenorhabditis elegans microRNA-directed anti-  
 CC microRNAs upon which anti-microRNAs of the invention may be based.

XX SQ Sequence 22 BP; 7 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 22;

Best Local Similarity 72.2%; Pred. No. 4.6e+03;

Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18

||||||| :||| |||  
 Db 3 CAUCAAGCTGGCUGUGA 20

RESULT 14

ADA00062/c

ID ADA00062 standard; RNA; 23 BP.

XX ADA00062;

XX 06-NOV-2003 (first entry)

XX D. melanogaster miRNA sequence mir-2a SEQ ID NO:59.

XX Drosophila melanogaster; human; mouse; microRNA; miRNA; cytostatic;  
 KW gene therapy; diagnostic; therapeutic; developmental modulator;  
 KW pathogenic modulator; cancer; B-cell chronic leukaemia;  
 KW tissue reprogramming; ss.

XX Drosophila melanogaster.

XX WO2003029459-A2.

XX 10-APR-2003.

XX 27-SEP-2002; 2002WO-EP010881.

28-SEP-2001; 2001EP-00123453.  
22-MAR-2002; 2002EP-00006712.  
26-JUL-2002; 2002EP-00016772.  
(PLAC ) MAX PLANCK GES FOERDERUNG.  
Tuschl T, Lagos-Quintana M, Lendeckel W, Meyer J, Rauhut R;  
WPI; 2003-381637/36.  
New nucleic acid molecule for diagnostic and therapeutic applications and as a marker or a modulator of developmental or pathogenic processes, e.g. cancer, comprises microRNAs of a Drosophila melanogaster, a human or a mouse.  
Claim 1; Page 26; 138pp; English.  
The present invention describes an isolated nucleic acid molecule (I) comprising a nucleotide sequence of Drosophila melanogaster, human or mouse microRNAs (miRNAs), or their precursors, a complement of it, a nucleotide sequence that has an affinity of at least 80 % to them or a nucleotide sequence that hybridises under stringent conditions to them. Also described: (1) a pharmaceutical composition containing the nucleic acid and, optionally, a carrier; and (2) identifying miRNA molecules or precursor molecules, comprising ligating 5'- and 3'-adapter molecules to the ends of a size-fractionated RNA population, reverse transcribing the adapter-containing RNA population and characterising the reverse transcription products. (I) has cytostatic activity, and can be used in gene therapy. The pharmaceutical composition is useful for diagnostic and therapeutic applications, and as a marker or a modulator of developmental or pathogenic processes, particularly of cancer (e.g. B-cell chronic leukaemia) or gene expression. The miRNA molecules may also be used in tissue reprogramming procedures. The present sequence represents an miRNA sequence from the present invention.  
Sequence 23 BP; 6 A; 6 C; 5 G; 0 T; 6 U; 0 Other;  
Query Match 73.3%; Score 13.2; DB 8; Length 23;  
Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0  
QY 1 CATCAAGGTGGCGGAGA 18  
||||| |||||  
Db 20 CATCAAGCTGGCTGTGA 3  
RESULT 15  
ADR83113/c  
ID ADR83113 standard; RNA; 23 BP.  
AC ADR83113;  
XX  
XX  
DT 02-DEC-2004 (first entry)  
XX  
XX Human miRNA oligo that modulates expression of human target mRNA Seq 15.  
DE  
XX human; ss; miRNA; microRNA; ontogenesis; cell therapy; cancer;  
KW immune disease; nerve disorder; amyotrophic lateral sclerosis;  
KW Parkinson's disease; Alzheimer's disease; inflammatory disease;  
KW siRNA silencing precursor; cycostatic; immunosuppressive; neurotropic;  
KW neuroprotective; antiinflammatory; immunotherapy.  
XX  
OS Homo sapiens.  
XX  
XX WO2004076622-A2.  
XX  
XX 10-SEP-2004.  
XX  
XX 10-FEB-2004; 2004WO-JP001433.  
XX  
XX 10-FEB-2003; 2003US-0445829P.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX WPI; 2005-075536/08.  
XX  
XX Enhancing the ability of a first strand of a RNAi agent to act as a guide  
PT strand in mediating RNAi for treating e.g., cancer by lessening the base  
PT pair strength between the 5' end of the first strand and the 3' end of a  
PT second strand.  
XX  
XX Disclosure; Fig 6B; 127pp; English.  
XX  
XX The invention relates to a novel method for enhancing the ability of a  
CC first strand of a RNAi agent to act as a guide strand in mediating RNAi.  
CC The method comprises reducing the base pair strength between the 5' end  
CC of the first strand and the 3' end of a second strand of the duplex, as  
CC compared to the base pair strength between the 3' end of the first strand  
CC and the 5' end of the second strand. The invention further comprises:  
CC enhancing the efficacy of a siRNA duplex comprising a sense and an  
CC antisense strand; promoting entry of a desired strand of an siRNA duplex  
CC into a RISC complex; enhancing silencing of a target mRNA; enhancing  
CC silencing of a target mRNA in a subject; decreasing silencing of an  
CC inadvertent target mRNA by a dsRNA agent comprising a sense strand and  
CC an antisense strand; an siRNA duplex comprising a sense strand and an  
CC antisense strand, where the base pair strength between the antisense  
CC strand 5' end and the sense strand 3' end is less than the base pair  
CC strength between the antisense strand 3' end and the sense strand 5' end,  
CC so that the antisense strand preferentially guides cleavage of a target  
CC mRNA; a composition comprising the RNAi agent or siRNA duplex formulated  
CC to facilitate entry of the RNAi agent or siRNA duplex into a cell; an  
CC engineered pre-miRNA comprising the RNAi agent or siRNA duplex; a primary  
CC -microRNA (pri-miRNA) comprising the pre-miRNA; a small hairpin RNA  
CC (shRNA) comprising a nucleotide sequence identical to the sense and  
CC antisense strand of the siRNA duplex; a vector encoding the miRNA, pre-  
CC miRNA or shRNA; a cell comprising the vector; and a transgene encoding  
CC the shRNA. The RNAi agent has cytostatic activity and may be used in gene  
CC therapy. The method is useful in enhancing the ability of a first strand  
CC of a RNAi agent to act as a guide strand in mediating RNAi for preparing  
CC a composition for treating or preventing a disease, e.g. cancer. This  
CC polynucleotide sequence represents an siRNA oligo strand used in the  
CC exemplification of the invention.  
XX  
SQ Sequence 23 BP; 6 A; 6 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 23;  
Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCGGAGA 18  
|||||  
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 17  
ADY31025/c  
ID ADY31025 standard; DNA; 23 BP.

XX AC ADY31025;

XX 05-MAY-2005 (first entry)

XX Micro RNA (miRNA)/human E2F3/EIF5A2/FOXAL-related DNA 7.

XX miRNA; micro RNA; RNA interference; gene silencing;  
KW E2F transcription factor 3; E2F3;  
KW eukaryotic translation initiation factor 5A2; EIF5A2; forkhead box A1;  
KW FOXAL; hepatocyte nuclear factor 3 alpha; HNF3alpha; ss.

XX Unidentified.

XX WO2005017145-A1.

XX 24-FEB-2005.

XX 12-AUG-2004; 2004WO-JP011624.

XX 13-AUG-2003; 2003JP-00293129.  
PR  
XX (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.  
PA (BITS-) BITS CO LTD.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX  
PI Barrero Roberto Antonio, Tamura T, Imanishi T, Gojobori T;  
PI Taira K, Kawasaki H;  
XX WPI; 2005-196094/20.  
XX  
XX Identifying a gene under regulation of functional RNA, involves setting  
PT ambiguity of different standards in conserved and unconserved region of  
PT functional RNA, searching for gene which is complementary to functional  
PT RNA.

XX Example 1; Fig 5; 38pp; Japanese.

XX The invention relates to a novel method for identifying or presuming a  
CC functional miRNA (micro RNA) molecule of base length of 16-25 and a gene  
CC which is regulated as a result of targeting by the miRNA. The method  
CC comprises determining and classifying the base sequences of functional  
CC RNA molecules into conserved and unconserved regions, setting ambiguities  
CC of different standards in these regions and searching for a candidate  
CC gene which has a base sequence complementary to the functional RNA  
CC molecule. The method of the invention may be useful for identifying a  
CC gene whose expression is under regulation by a functional RNA molecule of  
CC base length of 16-25. The method is thus useful for developing treatments  
CC for a disease or for treating a disease by controlling the biological  
CC function of the target gene. The current sequence is that of a micro RNA  
CC (miRNA)/human gene-related DNA of the invention. Specifically, human E2F  
CC transcription factor 3 (E2F3), eukaryotic translation initiation factor 3  
CC 5A2 (EIF5A2) and forkhead box A1 (FOXAL, hepatocyte nuclear factor 3  
CC alpha, HNF3alpha) are referred to in claim 9.

XX Sequence 23 BP; 6 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 23;  
Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCGGAGA 18  
|||||  
Db 20 CATCAAGCTGGCTGTGA 3

RESULT 18  
ADY31024/c  
ID ADY31024 standard; DNA; 23 BP.

XX AC ADY31024;

XX 05-MAY-2005 (first entry)

XX Micro RNA (miRNA)/human E2F3/EIF5A2/FOXAL-related DNA 6.

XX miRNA; micro RNA; RNA interference; gene silencing;  
KW E2F transcription factor 3; E2F3;  
KW eukaryotic translation initiation factor 5A2; EIF5A2; forkhead box A1;  
KW FOXAL; hepatocyte nuclear factor 3 alpha; HNF3alpha; ss.

XX Unidentified.

XX WO2005017145-A1.

XX 24-FEB-2005.

XX 12-AUG-2004; 2004WO-JP011624.

XX 13-AUG-2003; 2003JP-00293129.

XX (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.

PA (BITS-) BITS CO LTD.  
 XX (NRAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PI Barrero Roberto Antonio, Tamura T, Imanishi T, Gojobori T;  
 XX Taira K, Kawasaki H;  
 DR WPI; 2005-196094/20.  
 XX  
 XX Identifying a gene under regulation of functional RNA, involves setting  
 PT ambiguity of different standards in conserved and unconserved region of  
 PT functional RNA, searching for gene which is complementary to functional  
 PT RNA.  
 XX  
 XX Example 1; Fig 5; 38pp; Japanese.  
 XX  
 CC The invention relates to a novel method for identifying or presuming a  
 CC functional miRNA (micro RNA) molecule of base length of 16-25 and a gene  
 CC which is regulated as a result of targeting by the miRNA. The method  
 CC comprises determining and classifying the base sequences of functional  
 CC RNA molecules into conserved and unconserved regions, setting ambiguities  
 CC of different standards in these regions and searching for a candidate  
 CC gene which has a base sequence complementary to the functional RNA  
 CC molecule. The method of the invention may be useful for identifying a  
 CC gene whose expression is under regulation by a functional RNA molecule of  
 CC base length of 16-25. The method is thus useful for developing treatments  
 CC for a disease or for treating a disease by controlling the biological  
 CC function of the target gene. The current sequence is that of a micro RNA  
 CC (miRNA)/human gene-related DNA of the invention. Specifically, human E2F  
 CC transcription factor 3 (E2F3), eukaryotic translation initiation factor  
 CC SA2 (EIF5A2) and forkhead box A1 (FOXA1), hepatocyte nuclear factor 3  
 CC alpha, HNF3alpha) are referred to in claim 9.  
 XX  
 SQ Sequence 23 BP; 6 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 13.2; DB 14; Length 23;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CATCAAGGTGGCCGAGA 18  
 Db 20 CATCAAGGTGGCTGTGA 3  
 RESULT 19  
 ADF16111  
 ID ADF16111 standard; DNA; 42 BP.  
 AC ADF16111;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human albumin fusion protein-related PCR primer SeqID1198.  
 XX  
 KW albumin fusion protein; albumin activity; human serum albumin;  
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;  
 KW gene therapy; diabetes mellitus; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003060071-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 XX 23-DEC-2002; 2002WO-US040891.  
 XX  
 PR 21-DEC-2001; 2001US-0341811P.  
 PR 24-JAN-2002; 2002US-0350358P.  
 PR 28-JAN-2002; 2002US-0351360P.  
 PR 26-FEB-2002; 2002US-0359370P.  
 PR 28-FEB-2002; 2002US-0360000P.  
 PR 27-MAR-2002; 2002US-0367500P.  
 PR 08-APR-2002; 2002US-0370227P.  
 PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.  
 PR 28-MAY-2002; 2002US-0383123P.  
 PR 05-JUN-2002; 2002US-0385708P.  
 PR 10-JUL-2002; 2002US-0394625P.  
 PR 24-JUL-2002; 2002US-0398008P.  
 PR 09-AUG-2002; 2002US-0402131P.  
 PR 13-AUG-2002; 2002US-0402708P.  
 PR 18-SEP-2002; 2002US-0411355P.  
 PR 18-SEP-2002; 2002US-0411426P.  
 PR 02-OCT-2002; 2002US-0414984P.  
 PR 11-OCT-2002; 2002US-0417611P.  
 PR 23-OCT-2002; 2002US-0420246P.  
 PR 05-NOV-2002; 2002US-0423623P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (DELZ ) DELTA BIOTECHNOLOGY LTD.  
 PA (PRIN-) PRINCIPIA PHARM CORP.  
 XX  
 PI Ballance DV, Turner AJ, Rosen CA, Haseltine WA;  
 XX WPI; 2003-598517/56.  
 DR  
 PT New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.  
 XX  
 XX Example 4; SEQ ID NO 1198; 24pp; English.  
 XX  
 CC This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also  
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of  
 CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production of compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a PCR primer which may  
 CC be used for amplification of a DNA sequence encoding a therapeutic  
 CC protein which was fused with human albumin to create a novel albumin  
 CC fusion protein of the invention. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 42 BP; 8 A; 13 C; 17 G; 4 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 13.2; DB 10; Length 42;  
 Best Local Similarity 83.3%; Pred. No. 4.9e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CATCAAGGTGGCCGAGA 18  
 Db 13 CCTCAAGGTGGCGTAGA 30  
 RESULT 20  
 AAL32362  
 ID AAL32362 standard; DNA; 51 BP.  
 XX  
 AC AAL32362;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #5570.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinase; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.

```
XX OS Homo sapiens.
XX PN WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US035498.
XX PR 28-DEC-1999; 99US-0173419P.
XX PR 27-DEC-2000; 2000US-00173419.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX PT autoimmune diseases and infections.
XX PS Claim 1; Page 2991; 4143pp; English.
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX CC protein coupled receptors and thioesterases. The present sequence is one
XX CC such oligonucleotide. The oligonucleotides and the peptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of the proteins listed above.
XX CC Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms
XX SQ Sequence 51 BP; 21 A; 4 C; 9 G; 17 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 51;
Best Local Similarity 83.3%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
   || || || || || || || ||
Db 2 CACACAGATGCCGTGA 19

RESULT 21
AAS43685/C
ID AAS43685 standard; DNA; 68 BP.
AC AAS43685;
XX 18-DEC-2001 (first entry)
XX DE Corneodesmosin single nucleotide polymorphism #43.
XX KW Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX OS Homo sapiens.
XX PN WO200162788-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-GB000795.
XX PI Lee S, Lee S, Suh B, Chae W, Kim J, Lee J;

23-FEB-2000; 2000GB-00004312.
XX PA (OXAG-) OXAGEN LTD.
XX PI Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX DR WPI; 2001-570627/64.
XX CC Corneodesmosin protein and polynucleotide encoding it, having one or more
XX PT polymorphisms useful in treating, diagnosing or determining
XX PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX PT diseases.
XX PS Disclosure; Page 39; 60pp; English.
XX CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX CC encoding the corneodesmosin gene, where the gene comprises a base
XX CC substitution, deletion or insertion at one or more positions. (I) and
XX CC (II) are useful for screening for agents for use in prognosis, diagnosis
XX CC and treatment of individuals having or being susceptible to
XX CC corneodesmosin-mediated disease, by monitoring the reaction between the
XX CC molecules and the agents. The nucleotide and amino acid polymorphisms are
XX CC useful for diagnosing or determining subsequent treatment of the disease
XX CC mediated disease, which facilitates subsequent treatment of the disease
XX CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX CC are useful in diagnostic, prognostic or therapeutic methods and as
XX CC research tools for e.g. in drug screening. (II) is useful as probes or
XX CC primers for detecting an allele of the polymorphism or in the regulation
XX CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX CC screening DNA clone libraries for cells secreting the antigen. (II) is
XX CC useful as a model to investigate the role of corneodesmosin in normal
XX CC skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX CC invention
XX SQ Sequence 68 BP; 10 A; 19 C; 27 G; 11 T; 0 U; 1 Other;

Query Match 73.3%; Score 13.2; DB 5; Length 68;
Best Local Similarity 83.3%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
   || || || || || || || ||
Db 62 CATCCAGGTGGCCGAGA 45

RESULT 22
ADA37054/C
ID ADA37054 standard; DNA; 72 BP.
XX AC ADA37054;
XX 20-NOV-2003 (first entry)
XX DT Sim-2-CTLA4 3' PCR primer SEQ ID NO:16.
XX DE biomolecule transduction motif; SIM-2-BTM; biological response modifier;
XX KW drug delivery; vaccine; gene therapy; protein therapy; pharmaceutical;
XX KW PCR primer; ss.
XX OS Synthetic.
XX PN WO2003059940-A1.
XX PD 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-KR000121.
XX PR 19-JAN-2002; 2002KR-00003184.
XX PA (LEES/) LEE S.
XX PI Lee S, Lee S, Suh B, Chae W, Kim J, Lee J;
```

XX WPI; 2003-636699/60.

XX Novel Sim-2 biomolecule transduction motif peptide or its active

PT fragment, useful for transducing a biologically active, functional and/or

PT regulatory molecule e.g., DNA, RNA into prokaryotic or eukaryotic cells.

XX

XX Disclosure; Page 91; 94pp; English.

XX The present invention describes a biomolecule transduction motif

CC designated SIM-2-BTM. The SIM-2-BTM peptide has a potential to transduce

CC many biological response modifiers effectively into the cytoplasm,

CC intracellular organelles or nucleus of prokaryotic or eukaryotic cells in

CC vivo and in vitro, and the related technological methods for using SIM-2-

CC BTM. SIM-2-BTM can be used in drug delivery systems, for the development

CC of recombinant protein vaccines or DNA/RNA vaccines, in gene and protein

CC therapy, in the production of pharmacologically or medically useful

CC protein, or in pharmaceutical drug therapy. The present sequence

CC represents a primer which is used in the exemplification of the present

CC invention.

XX

XX Sequence 72 BP; 18 A; 16 C; 18 G; 20 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 72;

Best Local Similarity 83.3%; Pred. No. 5.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCGGAGA 18

|||||

Db 49 CATCAATGGCGCGCGGA 32

RESULT 23

ACF04460/c

ID ACF04460 standard; DNA; 72 BP.

XX ACF04460;

XX

XX 04-DEC-2003 (first entry)

DT

DE Biomolecule transduction motif Mph-1 vector pCDNA3-ZA1A2 primer #4.

XX

XX Transduction motif; MPH-1-BTM; Mph-1; drug delivery system;

KW protein vaccine; nucleic acid vaccine; gene therapy; protein therapy;

KW viricide; antibacterial; fungicide; cytostatic; antidiabetic;

KW immunosuppressive; PCR; primer; ss.

XX

OS Unidentified.

XX

XX WO2003059941-A1.

PN

XX

XX 24-JUL-2003.

XX

XX 20-JAN-2003; 2003WO-KR000122.

PF

XX

XX 19-JAN-2002; 2002KR-00003183.

PR

XX

XX (LEES/) LEE S.

PA

XX

XX Lee S, Lee S, Suh B, Chae W, Kim J, Lee J;

PI

XX

XX WPI; 2003-598502/56.

DR

XX

XX New biomolecule transduction motif Mph-1 peptide, useful for transducing

PT a biologically active, functional and/or regulatory molecule into

PT prokaryotic or eukaryotic cells, for drug delivery system, or gene and

PT protein therapy.

XX

XX Disclosure; Page 91; 93pp; English.

PS

XX The present invention relates to a biomolecule transduction motif Mph-1

CC peptide or its active fragment, which can be used for transducing a

CC biologically active, functional and/or regulatory molecule into

CC prokaryotic or eukaryotic cells. The biomolecule transduction motif Mph-1

CC peptide, its fusion protein, expression vector and biomolecule

CC transduction complex are useful for transducing a biologically active,

CC functional and/or regulatory molecule into prokaryotic or eukaryotic

CC cells. The Mph-1 peptide is also useful for drug delivery systems,

CC developing new recombinant protein or DNA/RNA vaccines against viruses,

CC bacteria, mold or various cancer cells, gene and protein therapy,

CC producing pharmacologically or medicinally useful proteins, or pharmaco-

CC medicinal drug therapy. In particular, the biomolecule transduction motif

CC Mph-1 peptide is useful for producing protein drugs with natural folding

CC structure and function e.g. Mph1-insulin fusion protein for treating

CC diabetes. The present sequence is a PCR primer used to amplify a vector

CC containing the coding sequence for the peptide of the invention

XX

XX Sequence 72 BP; 18 A; 16 C; 18 G; 20 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 72;

Best Local Similarity 83.3%; Pred. No. 5.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCGGAGA 18

|||||

Db 49 CATCAATGGCGCGCGGA 32

RESULT 24

ADR83553/c

ID ADR83553 standard; DNA; 76 BP.

XX ADR83553;

AC

XX

XX 02-DEC-2004 (first entry)

DT

XX

XX Human DNA related to regulating mammalian cells using miRNAs Seq 455.

DE

XX

XX human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;

KW immune disease; nerve disorder; amyotrophic lateral sclerosis;

KW Parkinson's disease; Alzheimer's disease; inflammatory disease;

KW siRNA silencing precursor; cytostatic; immunosuppressive; neurotropic;

KW neuroprotective; antiinflammatory; immunotherapy.

XX

OS Homo sapiens.

XX

XX WO2004076622-A2.

PN

XX

XX 10-SEP-2004.

PD

XX

XX 10-FEB-2004; 2004WO-JP001433.

PF

XX

XX 10-FEB-2003; 2003US-0445829P.

PR

XX

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA

XX

XX Taira K, Kawasaki H;

PI

XX

XX WPI; 2004-653393/63.

DR

XX

XX Modulating expression of a target gene in a cell, for treating cancer, an

PT immune disease, or a nerve disorder, comprises introducing into the cell

PT a polynucleotide that forms a duplex region with an mRNA transcribed from

PT the target gene.

PT

XX

XX Disclosure; SEQ ID NO 455; 865pp; English.

PS

XX

XX This invention relates to a novel method for modulating the expression of

CC a target gene in a cell. Specifically, it refers to the introduction into

CC a cell of a polynucleotide that forms a duplex region with an mRNA

CC transcribed from the target gene, where the duplex region comprises a

CC mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that

CC regulates mRNA at a post-transcriptional level. The present invention

CC describes a method for controlling ontogenesis of a mammal, function of a

CC mammalian cell, differentiation of a mammalian cell or viability of a

CC mammalian cell in the post-transcriptional phase, which comprises

CC introducing a plasmid vector comprising a promoter and nucleic acid  
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.  
CC Accordingly, it provides a cell therapy method for treating cancer,  
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,  
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease  
CC by introducing into the cell the miRNA, siRNA silencing precursor to the  
CC miRNA or the plasmid vector. As such, they can be developed into  
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,  
CC neurotropic, neuroprotective and antiinflammatory activities and hence can  
CC be used for immunotherapy. This polynucleotide sequence is a human DNA  
CC sequence related to the regulation of mammalian cells using miRNAs to  
CC modulate expression, given in an exemplification of the invention. NOTE:  
CC This sequence is given in the sequence listing but is not further  
CC referred to in the specification.

SQ Sequence 76 BP; 15 A; 18 C; 21 G; 22 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 13; Length 76;  
Best Local Similarity 83.3%; Pred. No. 5.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | |  
Db 68 CATCAAGGTGGCTGTGA 51

## RESULT 25

AAQ27315  
ID AAQ27315 standard; DNA; 18 BP.

XX AC AAQ27315;

XX DT 23-SEP-2004 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 01-FEB-1993 (first entry)

XX PCR primer Cbtaext for TCR Beta-Chain genes.

XX TCR, beta chain; rheumatoid arthritis; multiple sclerosis;  
KW autoimmune disease; diabetes; T-cell lymphoma; vaccination; immunisation;  
KW experimental allergic encephalomyelitis; ss.

XX Synthetic.

XX DN W09212996-A2.

XX PD 06-AUG-1992.

XX PF 21-JAN-1992; 92WO-US000482.

XX PR 22-JAN-1991; 91US-00644611.

XX PA (IMMU-) IMMUNE RESPONSE CORP.

XX PI Howell MD, Brostoff SW, Carlo DJ;

XX DR WPI; 1992-284600/34.

XX Treatment of auto-immune diseases e.g. rheumatoid arthritis - using  
PT vaccine contg. T-cell receptors from surface of T-cells which mediate the  
PT diseases.

XX Example 10; Page 48; 87pp; English.

XX This sequence represents a PCR primer used to amplify the T cell receptor  
CC beta chain genes in a two stage amplification reaction with nested pairs  
CC of primers. See also AAQ27310-7. (Updated on 25-MAR-2003 to correct PN  
CC field.)

CC Revised record issued on 23-SEP-2004 : Correction to keywords

XX Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | |

Db 5 AAGGTGGCCGAGA 17  
| | | | | | | | | | | | | | | | | | | |

Search completed: March 3, 2006, 08:00:20  
Job time : 124.534 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds  
(without alignments)  
1353.240 Million cell updates/sec

Title: US-10-655-801-19

Perfect score: 18  
Sequence: 1 catcaaggtgcccagaga 18

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/ECTUS COMB.seq.\*  
7: /cgn2\_6/prodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	77.8	25	3	US-09-396-196G-7331
C 2	14	77.8	25	3	US-09-396-196G-7332
C 3	14	77.8	25	3	US-09-396-196G-28185
C 4	13	72.2	18	2	US-08-466-860-53
C 5	13	72.2	18	3	US-08-472-040A-53
C 6	13	72.2	18	3	US-08-276-776-53
C 7	13	72.2	18	3	US-08-471-209-53
C 8	12.8	71.1	20	3	US-09-593-711A-216
C 9	12.8	71.1	25	3	US-09-396-196G-101443
C 10	12.8	71.1	26	3	US-08-943-731-282
C 11	12.8	71.1	52	2	US-08-629-039-5
C 12	12.4	68.9	19	3	US-09-696-791-874
C 13	12.4	68.9	24	3	US-09-518-914-24
C 14	12.4	68.9	25	3	US-09-396-196G-14358
C 15	12.4	68.9	25	3	US-09-396-196G-14359
C 16	12.4	68.9	27	2	US-08-808-793-31
C 17	12.4	68.9	45	3	US-09-518-914-18
C 18	12.4	68.9	50	3	US-10-131-827-4058
C 19	12.2	67.8	20	3	US-08-864-357F-19
C 20	12.2	67.8	22	3	US-09-954-736A-7
C 21	12.2	67.8	20	3	US-09-872-051-14
C 22	12.2	67.8	23	3	US-10-402-839A-2
C 23	12.2	67.8	23	3	US-10-402-839A-4
C 24	12.2	67.8	23	3	US-10-402-839A-8

Sequence 118719,	25	67.8	12.2	25	3	US-09-396-196G-118719	Sequence 118719,
Sequence 118720,	25	67.8	12.2	26	3	US-09-396-196G-118720	Sequence 118720,
Sequence 173, Appl	30	67.8	12.2	27	3	US-08-711-417C-173	Sequence 173, Appl
Sequence 14, Appl	30	67.8	12.2	28	3	US-08-733-622C-14	Sequence 14, Appl
Sequence 173, Appl	30	67.8	12.2	29	3	US-09-723-909-173	Sequence 173, Appl
Sequence 14, Appl	30	67.8	12.2	30	3	US-09-019-348-14	Sequence 14, Appl
Sequence 31745, A	17	66.7	12	31	3	US-09-396-196G-31745	Sequence 31745, A
Sequence 10250, A	17	65.6	11.8	32	3	US-09-866-108A-10250	Sequence 10250, A
Sequence 10251, A	17	65.6	11.8	33	3	US-09-866-108A-10251	Sequence 10251, A
Sequence 10252, A	17	65.6	11.8	34	3	US-09-866-108A-10252	Sequence 10252, A
Sequence 353, Appl	17	65.6	11.8	35	3	US-09-404-912-353	Sequence 353, Appl
Sequence 11, Appl	18	65.6	11.8	36	3	US-09-593-711A-11	Sequence 11, Appl
Sequence 156, Appl	20	65.6	11.8	37	3	US-09-488-671-156	Sequence 156, Appl
Sequence 43, Appl	20	65.6	11.8	38	3	US-09-865-993-43	Sequence 43, Appl
Sequence 26, Appl	21	65.6	11.8	39	3	US-09-896-915-26	Sequence 26, Appl
Sequence 3, Appl	22	65.6	11.8	40	3	US-09-068-880-3	Sequence 3, Appl
Sequence 1, Appl	24	65.6	11.8	41	3	US-09-011-608-1	Sequence 1, Appl
Sequence 1, Appl	24	65.6	11.8	42	3	US-09-722-348-1	Sequence 1, Appl
Sequence 12, Appl	24	65.6	11.8	43	3	US-09-600-031-12	Sequence 12, Appl
Sequence 15142, A	25	65.6	11.8	44	3	US-09-866-108A-15142	Sequence 15142, A
Sequence 15143, A	25	65.6	11.8	45	3	US-09-866-108A-15143	Sequence 15143, A
Sequence 15144, A	25	65.6	11.8	46	3	US-09-866-108A-15144	Sequence 15144, A
Sequence 15145, A	25	65.6	11.8	47	3	US-09-866-108A-15145	Sequence 15145, A
Sequence 15146, A	25	65.6	11.8	48	3	US-09-866-108A-15146	Sequence 15146, A
Sequence 15147, A	25	65.6	11.8	49	3	US-09-866-108A-15147	Sequence 15147, A
Sequence 15148, A	25	65.6	11.8	50	3	US-09-866-108A-15148	Sequence 15148, A
Sequence 15149, A	25	65.6	11.8	51	3	US-09-866-108A-15149	Sequence 15149, A
Sequence 15150, A	25	65.6	11.8	52	3	US-09-866-108A-15150	Sequence 15150, A
Sequence 15151, A	25	65.6	11.8	53	3	US-09-866-108A-15151	Sequence 15151, A
Sequence 15152, A	25	65.6	11.8	54	3	US-09-866-108A-15152	Sequence 15152, A
Sequence 66324, A	25	65.6	11.8	55	3	US-09-396-196G-66324	Sequence 66324, A
Sequence 105959,	25	65.6	11.8	56	3	US-09-396-196G-105959	Sequence 105959,
Sequence 1, Appl	29	65.6	11.8	57	3	US-08-440-566-1	Sequence 1, Appl
Sequence 27, Appl	29	65.6	11.8	58	3	US-09-896-915-27	Sequence 27, Appl
Sequence 3, Appl	30	65.6	11.8	59	2	US-08-321-613-3	Sequence 3, Appl
Sequence 70, Appl	30	65.6	11.8	60	3	US-08-938-830-70	Sequence 70, Appl
Sequence 1041, Ap	38	65.6	11.8	62	3	US-09-068-377-70	Sequence 1041, Ap
Sequence 1146, Ap	38	65.6	11.8	63	3	US-09-474-432B-1041	Sequence 1146, Ap
Sequence 1145, Ap	38	65.6	11.8	64	3	US-09-476-387-1045	Sequence 1145, Ap
Sequence 1040, Ap	38	65.6	11.8	65	3	US-09-476-387-1040	Sequence 1040, Ap
Sequence 3189, Ap	47	65.6	11.8	66	3	US-09-422-978-3189	Sequence 3189, Ap
Sequence 7469, Ap	50	65.6	11.8	67	3	US-10-131-827-7469	Sequence 7469, Ap
Sequence 8112, Ap	52	65.6	11.8	68	3	US-10-131-827-8112	Sequence 8112, Ap
Sequence 21, Appl	52	65.6	11.8	69	3	US-08-358-918-21	Sequence 21, Appl
Sequence 41, Appl	52	65.6	11.8	70	2	US-08-883-795A-21	Sequence 41, Appl
Sequence 43, Appl	55	65.6	11.8	71	3	US-09-386-642-41	Sequence 43, Appl
Sequence 42, Appl	55	65.6	11.8	72	3	US-09-386-642-42	Sequence 42, Appl
Sequence 44, Appl	55	65.6	11.8	73	3	US-09-386-642-44	Sequence 44, Appl
Sequence 5, Appl	56	65.6	11.8	74	3	US-09-386-642-44	Sequence 5, Appl
Sequence 18, Appl	70	65.6	11.8	75	2	US-08-893-795A-5	Sequence 18, Appl
Sequence 34, Appl	73	65.6	11.8	76	2	US-08-434-001-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	77	2	US-08-433-585-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	78	2	US-08-433-425-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	79	2	US-08-437-667-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	80	2	US-08-906-955-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	81	2	US-08-945-909-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	82	2	US-09-396-002A-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	83	2	US-10-077-319-34	Sequence 34, Appl
Sequence 34, Appl	73	65.6	11.8	84	2	PCT-US96-06060-34	Sequence 34, Appl
Sequence 26523, A	74	65.6	11.8	85	3	US-09-270-767-26523	Sequence 26523, A
Sequence 426, App	19	65.6	11.6	86	3	US-09-338-907-426	Sequence 426, App
Sequence 23, Appl	20	64.4	11.6	87	2	US-08-218-207-426	Sequence 23, Appl
Sequence 12, Appl	20	64.4	11.6	88	2	US-08-887-365-23	Sequence 12, Appl
Sequence 27, Appl	20	64.4	11.6	89	2	US-08-914-961-12	Sequence 27, Appl
Sequence 16, Appl	20	64.4	11.6	90	2	US-09-357-073-27	Sequence 16, Appl
Sequence 11, Appl	21	64.4	11.6	91	2	US-08-913-547-11	Sequence 11, Appl
Sequence 1746, Ap	21	64.4	11.6	92	3	US-09-657-472-1746	Sequence 1746, Ap
Sequence 6, Appl	23	64.4	11.6	93	3	US-10-402-839A-6	Sequence 6, Appl
Sequence 10, Appl	23	64.4	11.6	94	3	US-10-402-839A-10	Sequence 10, Appl

c 98 11.6 64.4 23 3 US-10-402-839A-12 Sequence 12, Appl  
c 99 11.6 64.4 23 3 US-10-402-839A-15 Sequence 15, Appl  
c 100 11.6 64.4 23 3 US-10-402-839A-21 Sequence 21, Appl

## ALIGNMENTS

## RESULT 1

US-09-396-196G-7331/C  
; Sequence 7331, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 60/100,678  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7331  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-7331

Query Match 77.8%; Score 14; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14  
| | | | | | | | | |  
Db 23 CATCAAGGTGGCC 10

## RESULT 2

US-09-396-196G-7332/C  
; Sequence 7332, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 60/100,678  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7332  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-7332

Query Match 77.8%; Score 14; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14  
| | | | | | | | | |  
Db 17 CATCAAGGTGGCC 4

## RESULT 3

US-09-396-196G-28185  
; Sequence 28185, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 28185  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-28185

Query Match 77.8%; Score 14; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AAAGTGGCGGAGA 18  
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Db 8 AAAGTGGCGGAGA 21

## RESULT 4

US-08-466-860-53  
; Sequence 53, Application US/08466860  
; Patent No. 5985552  
; GENERAL INFORMATION:  
; APPLICANT: HOWELL, MARK D.  
; APPLICANT: BROSTOFF, STEVEN W.  
; APPLICANT: CARLO, DENNIS J.  
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES  
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,860  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/813,867  
; FILING DATE: 24-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAMPBELL, CATHRYN  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IM 9107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-535-9001  
; TELEFAX: 619-535-8949  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-466-860-53

Query Match 72.2%; Score 13; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGGTGGCCGAGA 18
Db |||||

RESULT 5
US-08-472-040A-53
; Sequence 53, Application US/08472040A
; Patent No. 6090387
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,040A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 1641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-472-040A-53

Query Match 72.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGGTGGCCGAGA 18
Db |||||

RESULT 6
US-08-276-776-53
; Sequence 53, Application US/08276776
; Patent No. 6207645
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA: US/08/471,209  
;; FILING DATE: 24-DEC-1991  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION NUMBER: US 07/813,867  
;; FILING DATE: 24-DEC-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CAMPBELL, KATHRYN  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-IM 9107  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-535-9001  
;; TELEFAX: 619-535-8949  
;; INFORMATION FOR SEQ ID NO: 53:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-471-209-53

Query Match 72.2%; Score 13; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGGTGCCGCGA 18  
| | | | | | | | | |  
Db 5 AAGGTGCCGCGA 17

## RESULT 8

US-09-593-711A-216/c  
;; Sequence 216, Application US/09593711A  
;; Patent No. 6271030  
;; GENERAL INFORMATION:  
;; APPLICANT: Brett P. Monia  
;; APPLICANT: Madeline M. Butler  
;; APPLICANT: Jacqueline Wyatt  
;; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION  
;; FILE REFERENCE: RTS-0118  
;; CURRENT APPLICATION NUMBER: US/09/593,711A  
;; CURRENT FILING DATE: 2000-06-14  
;; NUMBER OF SEQ ID NOS: 244  
;; SEQ ID NO 216  
;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-593-711A-216

Query Match 71.1%; Score 12.8; DB 3; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGCGA 17  
| | | | | | | | | |  
Db 17 ATCAACGTGGCTGAG 2

## RESULT 9

US-09-396-196G-101443  
;; Sequence 101443, Application US/09396196G  
;; Patent No. 6821724  
;; GENERAL INFORMATION:  
;; APPLICANT: Michael Mittmann  
;; APPLICANT: David Mack  
;; APPLICANT: David Lockhart  
;; APPLICANT: Affymetrix, Inc.  
;; TITLE OF INVENTION: Methods of Genetic Analysis

;; FILE REFERENCE: 3101.1  
;; CURRENT APPLICATION NUMBER: US/09/396,196G  
;; CURRENT FILING DATE: 1999-09-15  
;; PRIOR APPLICATION NUMBER: 60/100,678  
;; PRIOR FILING DATE: 1998-09-17  
;; NUMBER OF SEQ ID NOS: 127806  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 101443  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: mus musculus  
;; US-09-396-196G-101443

Query Match 71.1%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGCGA 17  
| | | | | | | | | |  
Db 10 ATCAACGTGGCTGAG 25

## RESULT 10

US-08-943-731-282  
;; Sequence 282, Application US/08943731  
;; Patent No. 6265157  
;; GENERAL INFORMATION:  
;; APPLICANT: PROCKOP, DARWIN J.  
;; APPLICANT: SPOTILA, LORETTA D.  
;; APPLICANT: DELTAS, CONSTANTINOS D.  
;; APPLICANT: SEREDA, LARISA  
;; APPLICANT: LARSON, ANDREA W.  
;; APPLICANT: PACK, MICHAEL  
;; APPLICANT: COLIGE, ALAIN  
;; APPLICANT: EARLY, JAMES  
;; APPLICANT: KORKKO, JARMO  
;; APPLICANT: ALA-KOKKO, LEENA, et al.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
;; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
;; NUMBER OF SEQUENCES: 666  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
;; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
;; STREET: FLR  
;; CITY: PHILADELPHIA  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19103-7086  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/943,731  
;; FILING DATE: 03-OCT-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/212,322  
;; FILING DATE: 14-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/803,628  
;; FILING DATE: 03-DEC-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: DOYLE LEARY Ph.D., KATHRYN  
;; REGISTRATION NUMBER: 36,317  
;; REFERENCE/DOCKET NUMBER: 9598-27  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 215-965-1284  
;; TELEFAX: 215-567-2991  
;; TELEX: 831-494  
;; INFORMATION FOR SEQ ID NO: 282:  
;; SEQUENCE CHARACTERISTICS:

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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-282

Query Match      71.1%; Score 12.8; DB 3; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCAAAGTGGCCGAG 18
    |||||
Db 4 TCAAAGAGCCAGAGA 19

RESULT 11
US-08-629-039-5/c
; Sequence 5, Application US/08629039
; Patent No. 5958736
; GENERAL INFORMATION:
; APPLICANT: STAHL, Stefan
; APPLICANT: NYGREN, Per-Ake
; APPLICANT: HANSSON, Marianne
; APPLICANT: UHLEN, Mathias
; APPLICANT: NGUYEN, Thien N
; TITLE OF INVENTION: RECOMBINANT DNA CODING FOR SIGNAL
; TITLE OF INVENTION: PEPTIDE, SELECTIVE INTERACTING POLYPEPTIDE AND MEMBRANE
; TITLE OF INVENTION: ANCHORING SEQUENCE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/629,039
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/140,138
; FILING DATE: 03-NOV-1993
; APPLICATION NUMBER: SE 9101433-2
; FILING DATE: 13-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-629-039-5

Query Match      71.1%; Score 12.8; DB 2; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATCAAAGTGGCCGAG 17
    |||||
```

```
Db 37 ATCAAAGTGGCGGTG 22

RESULT 12
US-09-696-791-874
; Sequence 874, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 874
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk8 ribozyme binding site
US-09-696-791-874

Query Match      68.9%; Score 12.4; DB 3; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAG 17
    |||||
Db 4 CAAAGTGGCCGAG 17

RESULT 13
US-09-518-914-24
; Sequence 24, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-518-914-24

Query Match      68.9%; Score 12.4; DB 3; Length 24;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAGTGGCC 14
    |||||
Db 11 CACCAAGTGGCC 24

RESULT 14
US-09-396-196G-14358/c
; Sequence 14358, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
```

```
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14358
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-14358

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  AAAGTGGCCGAGA 18
    |||||||
Db   25 AACGGTGGCCGAGA 12

RESULT 15
US-09-396-196G-14359/c
; Sequence 14359, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14359
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-14359

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  AAAGTGGCCGAGA 18
    |||||||
Db   22 AACGGTGGCCGAGA 9

RESULT 16
US-08-808-793-31/c
; Sequence 31, Application US/08808793
; Patent No. 5858713
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Ingles, Patricia J.
; APPLICANT: Soderlund, David M.
; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
```

```
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,793
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,361
; FILING DATE: 24-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,649
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-808-793-31

Query Match      68.9%; Score 12.4; DB 2; Length 27;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  CATCAAGGTGGCC 14
    |||||||
Db   16 CCTCAAGGTGGCC 3

RESULT 17
US-09-518-914-18/c
; Sequence 18, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
; US-09-518-914-18

Query Match      68.9%; Score 12.4; DB 3; Length 45;
Best Local Similarity 92.9%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 CATCAAGGTGGCC 14  
 Db 34 CACCAAGGTGGCC 21

RESULT 18

US-10-131-827-4058  
 ; Sequence 4058, Application US/10131827  
 ; Patent No. 6905827  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
 ; FILE REFERENCE: 506612000120  
 ; CURRENT APPLICATION NUMBER: US/10/131,827  
 ; CURRENT FILING DATE: 2002-09-06  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 9090  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4058  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; OTHER INFORMATION: US-10-131-827-4058

Query Match 68.9%; Score 12.4; DB 3; Length 50;  
 Best Local Similarity 92.9%; Pred. No. 3.1e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAAGTGGCCGAGA 18  
 Db 17 AAAGTGGCCGAGA 30

RESULT 19

US-08-864-357F-19  
 ; Sequence 19, Application US/08864357F  
 ; Patent No. 6255281  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Claragen, Inc. & NIH  
 ; TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammato  
 ; FILE REFERENCE: 116142/2  
 ; CURRENT APPLICATION NUMBER: US/08/864,357F  
 ; CURRENT FILING DATE: 1997-05-28  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 19  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: mGAPDH-r primer sequence  
 ; US-08-864-357F-19

Query Match 67.8%; Score 12.2; DB 3; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17  
 Db 3 CATCGAAGTGGGAAGAG 19

RESULT 20

US-09-954-736A-7/c

; Sequence 7, Application US/09954736A  
 ; Patent No. 6689744  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Koepfen, Hartmut  
 ; APPLICANT: Ross, Sarajane  
 ; APPLICANT: Shou, Jianyong  
 ; TITLE OF INVENTION: NOTCH RECEPTOR AGONISTS AND USES  
 ; FILE REFERENCE: P1848R1  
 ; CURRENT APPLICATION NUMBER: US/09/954,736A  
 ; CURRENT FILING DATE: 2001-09-17  
 ; PRIOR APPLICATION NUMBER: US 60/234,674  
 ; PRIOR FILING DATE: 2000-09-22  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SEQ ID NO 7  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Oligonucleotide Probe  
 ; US-09-954-736A-7

Query Match 67.8%; Score 12.2; DB 3; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17  
 Db 17 CGTCAAGGTGGAGGAG 1

RESULT 21

US-09-872-051-14/c  
 ; Sequence 14, Application US/09872051  
 ; Patent No. 6825400  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Monsanto Co  
 ; APPLICANT: Behr, Carl  
 ; APPLICANT: Hironaka, Catherine  
 ; APPLICANT: Heck, Gregory  
 ; APPLICANT: You, Jinsong  
 ; TITLE OF INVENTION: Corn Event PV-ZMGT32 (nk603) and Composition and Methods for Dete  
 ; FILE REFERENCE: 38-21(52258)B  
 ; CURRENT APPLICATION NUMBER: US/09/872,051  
 ; CURRENT FILING DATE: 2001-06-01  
 ; PRIOR APPLICATION NUMBER: 60/213,567  
 ; PRIOR FILING DATE: 2000-06-22  
 ; PRIOR APPLICATION NUMBER: 60/241,215  
 ; PRIOR FILING DATE: 2000-10-13  
 ; PRIOR APPLICATION NUMBER: 60/240,014  
 ; PRIOR FILING DATE: 2000-10-13  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 14  
 ; LENGTH: 22  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: Source  
 ; LOCATION: (1)..(22)  
 ; OTHER INFORMATION: fully synthesized  
 ; US-09-872-051-14

Query Match 67.8%; Score 12.2; DB 3; Length 22;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18  
 Db 22 ATAAAGGTGGCCCAA 6

## RESULT 22

US-10-402-839A-2/c  
; Sequence 2, Application US/10402839A  
; Patent No. 6955883  
; GENERAL INFORMATION:  
; APPLICANT: Perlegen Sciences  
; TITLE OF INVENTION: Life Sciences Business Systems and Methods  
; FILE REFERENCE: 29202-704  
; CURRENT APPLICATION NUMBER: US/10/402,839A  
; CURRENT FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 10/107,508  
; PRIOR FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: exemplary allele with variants  
US-10-402-839A-2

Query Match 67.8%; Score 12.2; DB 3; Length 23;  
Best Local Similarity 82.4%; Pred. No. 3.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17  
| | | | | | | | | | | | | | | | | | | | |  
Db 21 CGTCAAGGTGGCCGAG 5

## RESULT 23

US-10-402-839A-4/c  
; Sequence 4, Application US/10402839A  
; Patent No. 6955883  
; GENERAL INFORMATION:  
; APPLICANT: Perlegen Sciences  
; TITLE OF INVENTION: Life Sciences Business Systems and Methods  
; FILE REFERENCE: 29202-704  
; CURRENT APPLICATION NUMBER: US/10/402,839A  
; CURRENT FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 10/107,508  
; PRIOR FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: exemplary allele with common variants grouped into haplotypes  
US-10-402-839A-4

Query Match 67.8%; Score 12.2; DB 3; Length 23;  
Best Local Similarity 82.4%; Pred. No. 3.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17  
| | | | | | | | | | | | | | | | | | | | |  
Db 21 CGTCAAGGTGGCCGAG 5

## RESULT 24

US-10-402-839A-8/c  
; Sequence 8, Application US/10402839A  
; Patent No. 6955883  
; GENERAL INFORMATION:  
; APPLICANT: Perlegen Sciences  
; TITLE OF INVENTION: Life Sciences Business Systems and Methods  
; FILE REFERENCE: 29202-704  
; CURRENT APPLICATION NUMBER: US/10/402,839A  
; CURRENT FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 10/107,508

; PRIOR FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: exemplary allele with common variants  
US-10-402-839A-8

Query Match 67.8%; Score 12.2; DB 3; Length 23;  
Best Local Similarity 82.4%; Pred. No. 3.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17  
| | | | | | | | | | | | | | | | | | | | |  
Db 21 CGTCAAGGTGGCCGAG 5

## RESULT 25

US-09-396-196G-118719/c  
; Sequence 118719, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 118719  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-118719

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 3.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | |  
Db 25 ACCAAAGGTGCCCAAGA 9

Search completed: March 3, 2006, 07:34:52  
Job time : 24.6441 secs





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97 12.8 71.1 25 8 US-10-719-900-346264 Sequence 346264,
98 12.8 71.1 25 8 US-10-719-900-393527 Sequence 393527,
99 12.8 71.1 25 8 US-10-719-900-393528 Sequence 393528,
c 100 12.8 71.1 25 8 US-10-719-900-437530 Sequence 437530,

ALIGNMENTS

RESULT 1
US-10-182-049-19
; Sequence 19, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-182-049-19

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCCGAGA 18
| | | | | | | | | | | | | | | |
Db 1 CATCAAGGTGCCGAGA 18

RESULT 2
US-10-719-900-244282
; Sequence 244282, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 244282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-244282

Query Match 80.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
| | | | | | | | | | | | |
Db 7 ATCAAGGTGCTGAG 22

RESULT 3
US-11-036-317-138400/c
```

```
; Sequence 138400, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 138400
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-138400

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCCGAGA 16
| | | | | | | | | | | | |
Db 16 CTTCAAGGTGCCGAGA 1

RESULT 4
US-11-036-317-203113
; Sequence 203113, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 203113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-203113

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
| | | | | | | | | | | | |
Db 8 ATCAAGGTGCCGAG 23

RESULT 5
US-11-036-317-231362
; Sequence 231362, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

SEQ ID NO 231362  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-11-036-317-231362

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17  
 |||||  
 Db 9 ATCAAAGGTGCCGAG 24

RESULT 6

US-11-036-317-270126  
 Sequence 270126, Application US/11036317  
 Publication No. US20050214823A1  
 GENERAL INFORMATION:  
 APPLICANT: Williams, Alan  
 APPLICANT: Blume, John  
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 CURRENT APPLICATION NUMBER: US/11/036,317  
 CURRENT FILING DATE: 2005-01-13  
 PRIOR APPLICATION NUMBER: US 60/536,639  
 PRIOR FILING DATE: 2004-01-13  
 NUMBER OF SEQ ID NOS: 991174  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 270126  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-11-036-317-270126

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17  
 |||||  
 Db 5 ATCAAAGGTGCCGAG 20

RESULT 7

US-11-036-317-340096  
 Sequence 340096, Application US/11036317  
 Publication No. US20050214823A1  
 GENERAL INFORMATION:  
 APPLICANT: Williams, Alan  
 APPLICANT: Blume, John  
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 CURRENT APPLICATION NUMBER: US/11/036,317  
 CURRENT FILING DATE: 2005-01-13  
 PRIOR APPLICATION NUMBER: US 60/536,639  
 PRIOR FILING DATE: 2004-01-13  
 NUMBER OF SEQ ID NOS: 991174  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 340096  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-11-036-317-340096

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17  
 |||||  
 Db 7 ATCAAAGGTGCCGAG 22

RESULT 8

US-11-036-317-364267/c  
 Sequence 364267, Application US/11036317  
 Publication No. US20050214823A1  
 GENERAL INFORMATION:  
 APPLICANT: Williams, Alan  
 APPLICANT: Blume, John  
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 CURRENT APPLICATION NUMBER: US/11/036,317  
 CURRENT FILING DATE: 2005-01-13  
 PRIOR APPLICATION NUMBER: US 60/536,639  
 PRIOR FILING DATE: 2004-01-13  
 NUMBER OF SEQ ID NOS: 991174  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 364267  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-11-036-317-364267

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAAGTGCCGCA 16  
 |||||  
 Db 16 CTTCAAAGTGCCCGA 1

RESULT 9

US-11-036-317-365442  
 Sequence 365442, Application US/11036317  
 Publication No. US20050214823A1  
 GENERAL INFORMATION:  
 APPLICANT: Williams, Alan  
 APPLICANT: Blume, John  
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 CURRENT APPLICATION NUMBER: US/11/036,317  
 CURRENT FILING DATE: 2005-01-13  
 PRIOR APPLICATION NUMBER: US 60/536,639  
 PRIOR FILING DATE: 2004-01-13  
 NUMBER OF SEQ ID NOS: 991174  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 365442  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-11-036-317-365442

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGTGCCGAG 17  
 |||||  
 Db 4 ATCAAAGGTGCCGAG 19

RESULT 10

US-11-036-317-366373  
 Sequence 366373, Application US/11036317  
 Publication No. US20050214823A1  
 GENERAL INFORMATION:  
 APPLICANT: Williams, Alan  
 APPLICANT: Blume, John  
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 CURRENT APPLICATION NUMBER: US/11/036,317  
 CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 366373  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-366373

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17  
Db 6 ATCAAGGTGCCGAG 21

## RESULT 11

US-11-036-317-895040  
; Sequence 895040, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 895040

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-895040

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17  
Db 9 ATCAAGGTGCCGAG 24

## RESULT 12

US-11-036-317-957650  
; Sequence 957650, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 957650

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-957650

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17  
Db 7 ATCAAGGTGCCGAG 22

## RESULT 13

US-11-036-317-972134  
; Sequence 972134, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 972134

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-972134

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17  
Db 4 ATCAAGGTGCCGAG 19

## RESULT 14

US-11-036-317-972700  
; Sequence 972700, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 972700

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-972700

Query Match 80.0%; Score 14.4; DB 10; Length 25;  
Best Local Similarity 93.8%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17  
Db 6 ATCAAGGTGCCGAG 21

## RESULT 15

US-10-809-189-7331/C  
; Sequence 7331, Application US/10809189  
; Publication No. US20050048531A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189  
 ; PRIOR FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7331  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-809-189-7331

Query Match 77.8%; Score 14; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCC 14  
 |||||  
 DB 23 CATCAAGGTGGCC 10

RESULT 16  
 US-10-809-189-7332/c  
 ; Sequence 7332, Application US/10809189  
 ; Publication No. US20050048531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189  
 ; PRIOR FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7332  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-809-189-7332

Query Match 77.8%; Score 14; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCC 14  
 |||||  
 DB 17 CATCAAGGTGGCC 4

RESULT 17  
 US-10-809-189-28185  
 ; Sequence 28185, Application US/10809189  
 ; Publication No. US20050048531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189

; CURRENT FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28185  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-809-189-28185

Query Match 77.8%; Score 14; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAGTGGCCGAGA 18  
 |||||  
 DB 8 AAAGTGGCCGAGA 21

RESULT 18  
 US-10-956-157-202499/c  
 ; Sequence 202499, Application US/10956157  
 ; Publication No. US20050118625A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William  
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
 ; FILE REFERENCE: 031896-043000 (AM 101081)  
 ; CURRENT APPLICATION NUMBER: US/10/956,157  
 ; CURRENT FILING DATE: 2004-10-04  
 ; NUMBER OF SEQ ID NOS: 319805  
 ; SOFTWARE: Patent version 3.2  
 ; SEQ ID NO 202499  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Probe Sequence  
 US-10-956-157-202499

Query Match 77.8%; Score 14; DB 9; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCC 14  
 |||||  
 DB 18 CATCAAGGTGGCC 5

RESULT 19  
 US-11-036-317-95923  
 ; Sequence 95923, Application US/11036317  
 ; Publication No. US20050214823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Williams, Alan  
 ; APPLICANT: Blume, John  
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
 ; FILE REFERENCE: 3654.1  
 ; CURRENT APPLICATION NUMBER: US/11/036,317  
 ; CURRENT FILING DATE: 2005-01-13  
 ; PRIOR APPLICATION NUMBER: US 60/536,639  
 ; PRIOR FILING DATE: 2004-01-13  
 ; NUMBER OF SEQ ID NOS: 991174  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 95923  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-11-036-317-95923

Query Match 77.8%; Score 14; DB 10; Length 25;

```
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
    |||||
Db 3 CATCAAGGTGGCC 16
    |||||

RESULT 20
US-10-719-900-151203/c
; Sequence 151203, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-151203

Query Match 76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
    |||||
Db 22 CATCAAGGTGGCTAAG 6
    |||||

RESULT 21
US-10-719-900-819413/c
; Sequence 819413, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 819413
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-819413

Query Match 76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
    |||||
Db 22 CATCAATTTGGCCGAG 6
    |||||

RESULT 22
US-10-719-900-971153/c
; Sequence 971153, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 971153
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-971153

Query Match 76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
    |||||
Db 22 CATCAATTTGGCCGAG 6
    |||||

RESULT 23
US-11-036-317-909425/c
; Sequence 909425, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 909425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-909425

Query Match 76.7%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAGA 18
    |||||
Db 20 AACAAAGTGGCAGAGA 4
    |||||

RESULT 24
US-11-036-317-939953/c
; Sequence 939953, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 939953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-939953
```

Query Match 76.7%; Score 13.8; DB 10; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18  
 | | | | | | | | | | | | | | | | | | | | |  
 Db 22 AACAAAGGTGGCAGAGA 6

RESULT 25

US-10-775-204-1955  
 ; Sequence 1955, Application US/10775204  
 ; Publication No. US20050186664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen, Craig A.  
 ; APPLICANT: Haseltine, William A.  
 ; APPLICANT: Balance, David J.  
 ; APPLICANT: Turner, Andrew J.  
 ; TITLE OF INVENTION: Albumin Fusion Proteins  
 ; FILE REFERENCE: PF564  
 ; CURRENT APPLICATION NUMBER: US/10/775,204  
 ; CURRENT FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: 60/341,811  
 ; PRIOR FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: 60/360,000  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: 60/378,950  
 ; PRIOR FILING DATE: 2002-05-10  
 ; PRIOR APPLICATION NUMBER: 60/398,008  
 ; PRIOR FILING DATE: 2002-07-24  
 ; PRIOR APPLICATION NUMBER: 60/411,355  
 ; PRIOR FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: 60/414,984  
 ; PRIOR FILING DATE: 2002-10-02  
 ; PRIOR APPLICATION NUMBER: 60/417,611  
 ; PRIOR FILING DATE: 2002-10-11  
 ; PRIOR APPLICATION NUMBER: 60/420,246  
 ; PRIOR FILING DATE: 2002-10-23  
 ; PRIOR APPLICATION NUMBER: 60/423,623  
 ; PRIOR FILING DATE: 2002-11-05  
 ; PRIOR APPLICATION NUMBER: 60/351,360  
 ; PRIOR FILING DATE: 2002-01-28  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 2222  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 1955  
 ; LENGTH: 36  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-775-204-1955

Query Match 76.7%; Score 13.8; DB 9; Length 36;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18  
 | | | | | | | | | | | | | | | | | | | | |  
 Db 15 ATCAAGGTGGCGTAGA 31

Search completed: March 3, 2006, 08:48:46  
 Job time : 223.11 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds  
(without alignments)  
403.294 Million cell updates/sec

Title: US-10-655-801-19

Perfect score: 18

Sequence: 1 catcaagggtgcgcgaga 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA New.\*  
1: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
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12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred., No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	77.8	25	12	US-11-121-849-16738
C 2	14	77.8	25	12	US-11-121-849-31257
C 3	13.8	76.7	19	10	US-11-101-244-1487950
C 4	13.8	76.7	19	10	US-11-101-244-151236
C 5	13.8	76.7	19	10	US-11-101-244-1487950
C 6	13.8	76.7	19	10	US-11-101-244-1487950
C 7	13.8	76.7	19	10	US-11-101-244-151236
C 8	13.8	76.7	19	10	US-11-101-244-151236
C 9	13.4	74.4	19	10	US-11-101-244-889148
C 10	13.4	74.4	19	10	US-11-101-244-889148
C 11	13.4	74.4	19	10	US-11-101-244-936191
C 12	13.4	74.4	19	10	US-11-101-244-936569
C 13	13.4	74.4	19	10	US-11-101-244-936596
C 14	13.4	74.4	19	10	US-11-101-244-980471
C 15	13.4	74.4	19	10	US-11-101-244-621129
C 16	13.4	74.4	19	10	US-11-101-244-889148
C 17	13.4	74.4	19	10	US-11-101-244-889148
C 18	13.4	74.4	19	10	US-11-101-244-936191
C 19	13.4	74.4	19	10	US-11-101-244-936569
C 20	13.4	74.4	19	10	US-11-101-244-936596

19	11	US-11-083-784-980471	74.4	21	13.4
20	8	US-10-310-914A-280157	74.4	22	13.4
21	8	US-10-310-914A-280052	74.4	23	13.4
22	12	US-11-121-849-252474	74.4	24	13.4
23	12	US-11-175-859-105506	74.4	25	13.4
24	10	US-11-101-244-37909	73.3	26	13.2
25	10	US-11-101-244-75316	73.3	27	13.2
26	10	US-11-101-244-666336	73.3	28	13.2
27	10	US-11-101-244-854687	73.3	29	13.2
28	10	US-11-101-244-854687	73.3	30	13.2
29	10	US-11-101-244-1195260	73.3	31	13.2
30	10	US-11-101-244-1195260	73.3	32	13.2
31	10	US-11-101-244-1195260	73.3	33	13.2
32	10	US-11-101-244-1195260	73.3	34	13.2
33	10	US-11-101-244-1195260	73.3	35	13.2
34	10	US-11-101-244-1195260	73.3	36	13.2
35	10	US-11-101-244-1195260	73.3	37	13.2
36	10	US-11-101-244-1195260	73.3	38	13.2
37	10	US-11-101-244-1195260	73.3	39	13.2
38	10	US-11-101-244-1195260	73.3	40	13.2
39	10	US-11-101-244-1195260	73.3	41	13.2
40	10	US-11-101-244-1195260	73.3	42	13.2
41	10	US-11-101-244-1195260	73.3	43	13.2
42	10	US-11-101-244-1195260	73.3	44	13.2
43	10	US-11-101-244-1195260	73.3	45	13.2
44	10	US-11-101-244-1195260	73.3	46	13.2
45	10	US-11-101-244-1195260	73.3	47	13.2
46	10	US-11-101-244-1195260	73.3	48	13.2
47	10	US-11-101-244-1195260	73.3	49	13.2
48	10	US-11-101-244-1195260	73.3	50	13.2
49	10	US-11-101-244-1195260	73.3	51	13.2
50	10	US-11-101-244-1195260	73.3	52	13.2
51	10	US-11-101-244-1195260	73.3	53	12.8
52	10	US-11-101-244-1195260	73.3	54	12.8
53	10	US-11-101-244-1195260	73.3	55	12.8
54	10	US-11-101-244-1195260	73.3	56	12.8
55	10	US-11-101-244-1195260	73.3	57	12.8
56	10	US-11-101-244-1195260	73.3	58	12.8
57	10	US-11-101-244-1195260	73.3	59	12.8
58	10	US-11-101-244-1195260	73.3	60	12.8
59	10	US-11-101-244-1195260	73.3	61	12.8
60	10	US-11-101-244-1195260	73.3	62	12.8
61	10	US-11-101-244-1195260	73.3	63	12.8
62	10	US-11-101-244-1195260	73.3	64	12.8
63	10	US-11-101-244-1195260	73.3	65	12.8
64	10	US-11-101-244-1195260	73.3	66	12.8
65	10	US-11-101-244-1195260	73.3	67	12.8
66	10	US-11-101-244-1195260	73.3	68	12.8
67	10	US-11-101-244-1195260	73.3	69	12.8
68	10	US-11-101-244-1195260	73.3	70	12.8
69	10	US-11-101-244-1195260	73.3	71	12.8
70	10	US-11-101-244-1195260	73.3	72	12.8
71	10	US-11-101-244-1195260	73.3	73	12.8
72	10	US-11-101-244-1195260	73.3	74	12.8
73	10	US-11-101-244-1195260	73.3	75	12.8
74	10	US-11-101-244-1195260	73.3	76	12.8
75	10	US-11-101-244-1195260	73.3	77	12.8
76	10	US-11-101-244-1195260	73.3	78	12.8
77	10	US-11-101-244-1195260	73.3	79	12.8
78	10	US-11-101-244-1195260	73.3	80	12.8
79	10	US-11-101-244-1195260	73.3	81	12.8
80	10	US-11-101-244-1195260	73.3	82	12.8
81	10	US-11-101-244-1195260	73.3	83	12.8
82	10	US-11-101-244-1195260	73.3	84	12.8
83	10	US-11-101-244-1195260	73.3	85	12.8
84	10	US-11-101-244-1195260	73.3	86	12.8
85	10	US-11-101-244-1195260	73.3	87	12.8
86	10	US-11-101-244-1195260	73.3	88	12.8
87	10	US-11-101-244-1195260	73.3	89	12.8
88	10	US-11-101-244-1195260	73.3	90	12.8
89	10	US-11-101-244-1195260	73.3	91	12.8
90	10	US-11-101-244-1195260	73.3	92	12.8
91	10	US-11-101-244-1195260	73.3	93	12.4
92	10	US-11-101-244-1195260	73.3	94	12.4
93	10	US-11-101-244-1195260	73.3	95	68.9

Sequence 980471, Sequence 582157, Sequence 280052, Sequence 252474, Sequence 105506, Sequence 37909, A Sequence 75316, A Sequence 666336, Sequence 854687, Sequence 1077321, Sequence 1195260, Sequence 1195287, Sequence 1511903, Sequence 75316, A Sequence 666336, Sequence 854687, Sequence 1077321, Sequence 1195260, Sequence 1195287, Sequence 1511903, Sequence 1511903, Sequence 1183687, Sequence 148460, Sequence 160392, Sequence 216034, Sequence 489173, Sequence 203182, Sequence 203196, Sequence 203201, Sequence 1183667, Sequence 138452, Sequence 9011, Ap Sequence 530475, Sequence 530575, Sequence 530678, Sequence 530777, Sequence 64328, Sequence 803672, Sequence 1100478, Sequence 120141, Sequence 1207343, Sequence 1426795, Sequence 1488009, Sequence 530475, Sequence 530575, Sequence 530678, Sequence 530777, Sequence 64328, Sequence 803672, Sequence 1100478, Sequence 120141, Sequence 1207343, Sequence 1426795, Sequence 1488009, Sequence 216, App Sequence 445512, Sequence 104, App Sequence 1124735, Sequence 818764, Sequence 107844, Sequence 107845, Sequence 201076, Sequence 381162, Sequence 381163, Sequence 397343, Sequence 176741, Sequence 282453, Sequence 282457, Sequence 60245, A Sequence 8, Appli Sequence 6851, Ap Sequence 518464, Sequence 166948,

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94 12.4 68.9 19 10 US-11-101-244-28799 Sequence 28799, A
95 12.4 68.9 19 10 US-11-101-244-28899 Sequence 28899, A
c 96 12.4 68.9 19 10 US-11-101-244-37910 Sequence 37910, A
c 97 12.4 68.9 19 10 US-11-101-244-37928 Sequence 37928, A
98 12.4 68.9 19 10 US-11-101-244-296983 Sequence 296983,
99 12.4 68.9 19 10 US-11-101-244-296989 Sequence 296989,
100 12.4 68.9 19 10 US-11-101-244-297040 Sequence 297040,

ALIGNMENTS

RESULT 1
US-11-121-849-16738/c
; Sequence 16738, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-16738

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCC 14
Db 16 CATCAAGGTGCC 3

RESULT 2
US-11-121-849-31257/c
; Sequence 31257, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31257
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-31257

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCC 14
Db 16 CATCAAGGTGCC 3

RESULT 3
US-11-121-849-16738/c
; Sequence 16738, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-16738

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCC 14
Db 16 CATCAAGGTGCC 3
```

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US-11-101-244-1487950/c
; Sequence 1487950, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1487950
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1487950

Query Match 76.7%; Score 13.8; DB 10; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCCGAG 17
Db 18 CATCAAGGCGCTGAG 2

RESULT 4
US-11-101-244-1515236/c
; Sequence 1515236, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1515236

Query Match 76.7%; Score 13.8; DB 10; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGCCGAG 17
Db 18 CATCAAGGAGCGCCGAG 2

RESULT 5
US-11-083-784-1487950/c
```

```

; Sequence 1487950, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1487950
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1487950

```

```

Query Match          76.7%; Score 13.8; DB 11; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 CATCAAGGTGGCCGAG 17
Db 18 CATCAAGGTGGCTGAG 2

```

```

RESULT 6
US-11-083-784-1515236/c
; Sequence 1515236, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1515236

```

```

Query Match          76.7%; Score 13.8; DB 11; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 CATCAAGGTGGCCGAG 17
Db 18 CATCAAGGTGGCTGAG 2

```

```

RESULT 7
US-11-121-849-234566
; Sequence 234566, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 234566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-234566

```

```

Query Match          76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 CATCAAGGTGGCCGAG 17
Db 9 CCTCAAGGTGGCTGAG 25

```

```

RESULT 8
US-11-101-244-621129
; Sequence 621129, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 621129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-621129

```

```

Query Match          74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 CAAAGGTGGCCGAGA 18
Db 4 CCAGGUGGCCGAGA 18

```

```

RESULT 9
US-11-101-244-889148
; Sequence 889148, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 889148  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-889148

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | |  
Db 4 CAAAGGUGGCCGAGA 18

RESULT 10  
US-11-101-244-889168  
; Sequence 889168, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmaco, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 889168  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-889168

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 CAAAGGUGGCCGAGA 15

RESULT 11  
US-11-101-244-926191  
; Sequence 926191, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmaco, Inc.  
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 926191  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-926191

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAAGGUGGCCGAGA 18

RESULT 12  
US-11-101-244-956569  
; Sequence 956569, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmaco, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 956569  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-956569

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAAGGUGGCCGAGA 18

RESULT 13  
US-11-101-244-956596  
; Sequence 956596, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmaco, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 956596  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-956596

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 CCAAGGUGGCCGAGA 17

RESULT 14  
US-11-101-244-980471  
; Sequence 980471, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 980471  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-980471

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAAGGUGGCCGAGA 18

RESULT 15  
US-11-083-784-621129  
; Sequence 621129, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 621129  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-621129

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAAGGUGGCCGAGA 18

RESULT 16  
US-11-083-784-889148  
; Sequence 889148, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 889148  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-889148

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CCAAGGUGGCCGAGA 18

RESULT 17  
US-11-083-784-889168  
; Sequence 889168, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.

```
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 889168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-889168

Query Match      74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
   |||||:|||||
Db 1 CAAAGGUGGCCGAGA 15

RESULT 18
US-11-083-784-926191
; Sequence 926191, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 926191
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-926191

Query Match      74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
   |||||:|||||
Db 4 CCAAGGUGGCCGAGA 18

RESULT 19
US-11-083-784-956569
; Sequence 956569, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-956569

Query Match      74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
   |||||:|||||
Db 3 CCAAGGUGGCCGAGA 17
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-956569

Query Match      74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
   |||||:|||||
Db 4 CCAAGGUGGCCGAGA 18

RESULT 20
US-11-083-784-956596
; Sequence 956596, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956596
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-956596

Query Match      74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
   |||||:|||||
Db 3 CCAAGGUGGCCGAGA 17
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RESULT 21  
US-11-083-784-980471  
; Sequence 980471, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 980471  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-980471

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CAAAGTGGCCGAGA 18  
|||:|||||  
Db 4 CCAAGGUGGCCGAGA 18

RESULT 22  
US-10-310-914A-582157  
; Sequence 582157, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 582157  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-582157

Query Match 74.4%; Score 13.4; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CATCAAGGTGGCCG 15  
|:|||||  
Db 1 CCUCAAGGUGGCCG 15

RESULT 23  
US-10-310-914A-280052  
; Sequence 280052, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 280052  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-280052

Query Match 74.4%; Score 13.4; DB 8; Length 23;  
Best Local Similarity 86.7%; Pred. No. 4.4e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CAAAGTGGCCGAGA 18  
|||:|||||  
Db 7 CAGAGGUGGCCGAGA 21

RESULT 24  
US-11-121-849-252474/c  
; Sequence 252474, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 252474  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-252474

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 CAAAGTGGCCGAGA 18  
|||:|||||  
Db 18 CAAAGTGGCCGAGA 4

RESULT 25  
US-11-175-859-105506/c  
; Sequence 105506, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 105506  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-105506

Query Match 74.4%; Score 13.4; DB 12; Length 50;  
 Best Local Similarity 82.4%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAGA 18  
 |||||:|||||  
 Db 33 ATCAAGRTGGCTAAA 17

Search completed: March 3, 2006, 07:56:43  
 Job time : 98.0559 secs



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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds  
(without alignments)  
855.220 Million cell updates/sec

Title: US-10-655-801-19

Perfect score: 18

Sequence: 1 catcaaggtgcccagaga 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hic: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_gssi: \*  
10: gb\_gss2: \*  
11: gb\_gss3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	82.2	72	9	CC556903 CH240_464
2	13.8	76.7	58	3	BM434781 JPT13G10
3	13.4	74.4	43	10	CL982875 GC0098_T1
4	13.4	74.4	53	10	CG800410 1118012A0
5	13.4	74.4	60	10	CG726326 1118089E0
6	13.4	74.4	63	10	CG806795 1118074A0
7	13.4	74.4	69	10	CG020333 GC0591_T1
8	13.2	73.3	59	11	DME426975
9	13.2	73.3	61	10	CG802312
10	12.8	71.1	53	9	AZ339975
11	12.8	71.1	64	1	AA646597 ve46e05.r
12	12.8	71.1	64	1	AI624617 te69b07.x
13	12.8	71.1	78	9	AZ621111
14	12.4	68.9	45	3	BJ016067
15	12.4	68.9	57	1	AV834194
16	12.4	68.9	71	10	CG591414
17	12.4	68.9	71	1	AW164603
18	12.4	68.9	74	10	CG514254
19	12.4	68.9	77	10	CG510224
20	12.4	68.9	79	3	BP133993
21	12.2	67.8	29	10	CZ487115
22	12.2	67.8	31	9	BH850478

C 23	12.2	67.8	56	10	CZ483104
C 24	12.2	67.8	59	2	BG409364
C 25	12.2	67.8	59	10	CG575872
C 26	12.2	67.8	65	1	AA827028
C 27	12.2	67.8	66	2	BG116020
C 28	12.2	67.8	67	11	CR278093
C 29	12.2	67.8	74	10	CG729734
C 30	12.2	67.8	78	1	AI523075
C 31	12.2	67.8	78	2	BG910496
C 32	12.2	67.8	79	11	CR254716
C 33	12.2	67.8	80	10	CG527496
C 34	12.2	67.8	80	11	CR190533
C 35	12.2	66.7	50	1	AUI06266
C 36	12.2	66.7	55	9	AZ776193
C 37	12.2	66.7	60	6	CD944560
C 38	12.2	66.7	75	10	CG337827
C 39	12.2	66.7	76	8	H58746
C 40	11.8	65.6	39	9	AZ384591
C 41	11.8	65.6	40	10	AL766247
C 42	11.8	65.6	41	9	AZ410968
C 43	11.8	65.6	50	1	AUI02883
C 44	11.8	65.6	52	9	BH221325
C 45	11.8	65.6	52	9	BH626197
C 46	11.8	65.6	53	9	B00363
C 47	11.8	65.6	59	10	CG053729
C 48	11.8	65.6	70	11	CR162837
C 49	11.8	65.6	71	9	BH894176
C 50	11.8	65.6	76	1	AA457044
C 51	11.8	65.6	76	7	CV466027
C 52	11.8	65.6	76	10	BX895654
C 53	11.8	65.6	77	10	CG064212
C 54	11.8	65.6	79	1	AA223105
C 55	11.8	65.6	79	1	AA553236
C 56	11.6	64.4	37	10	CG712023
C 57	11.6	64.4	49	10	CG783969
C 58	11.6	64.4	50	1	AA717501
C 59	11.6	64.4	52	11	CR359266
C 60	11.6	64.4	53	10	CG135706
C 61	11.6	64.4	54	9	BH628620
C 62	11.6	64.4	55	1	AA572472
C 63	11.6	64.4	55	2	BE732284
C 64	11.6	64.4	57	9	B01965
C 65	11.6	64.4	59	1	AA283228
C 66	11.6	64.4	61	1	AI570241
C 67	11.6	64.4	65	8	W75049
C 68	11.6	64.4	65	9	AZ470048
C 69	11.6	64.4	66	9	AZ809396
C 70	11.6	64.4	69	8	CG571160
C 71	11.6	64.4	70	8	Z19901
C 72	11.6	64.4	70	9	BH906540
C 73	11.6	64.4	71	9	CG885346
C 74	11.6	64.4	73	6	CF652273
C 75	11.6	64.4	76	1	AI873248
C 76	11.6	64.4	77	10	AG189240
C 77	11.6	64.4	77	10	CG031050
C 78	11.6	64.4	79	1	AW420201
C 79	11.6	64.4	79	5	BO756208
C 80	11.6	64.4	79	11	CR359149
C 81	11.4	63.3	20	9	AZ964660
C 82	11.4	63.3	43	1	AV952014
C 83	11.4	63.3	43	10	CL211120
C 84	11.4	63.3	52	5	BX763192
C 85	11.4	63.3	58	1	AJ747306
C 86	11.4	63.3	60	10	CZ490547
C 87	11.4	63.3	61	10	CZ490549
C 88	11.4	63.3	66	8	DR038246
C 89	11.4	63.3	66	5	BQ586352
C 90	11.4	63.3	68	11	CR147982
C 91	11.4	63.3	69	10	CG509165
C 92	11.4	63.3	70	10	AL755545
C 93	11.4	63.3	71	9	BZ290183
C 94	11.4	63.3	72	9	BZ290481
C 95	11.4	63.3	73	9	BH847153

CZ483104	f00637-5p
BG409364	gb91e01.y
CG575872	OST210072
AA827028	n-89h10.s
BG116020	602318007
CR278093	Reverse s
CG729734	1119114D0
AI523075	ar68b07.x
BG910496	602806182
CR254716	Reverse s
CG527496	OST105496
CR190533	Reverse s
AUI06266	AUI06266
AZ776193	2M0009G10
CD944560	RDK_47 Ge
CG337827	104_837_1
H58746	yr25h02_el_1
AZ384591	1M0142K09
AL766247	Arabidops
AZ410968	1M0183B17
AUI02883	AUI02883
BH221325	1006100F0
BH626197	1007112A1
B00363	CSRL-108d3-
CG053729	104_294_1
CR162837	Forward s
BH894176	3526_1_28
AA457044	aa38d02.s
CV466027	MdfrtC3095
BX895654	Arabidops
CG064212	104_310_1
AA223105	zr0508.r
AA553236	vk89d12.s
CG712023	1119023G0
CG783969	01S0720-0
AA717501	vu22d09.r
CR359266	Arabidops
CG135706	104_520_1
BH628620	1007083H1
AA572472	vl82d07.r
BE732284	601570267
B01965	CSRL-144A5-
AA283228	CJC007 HT
AI570241	to76g04.x
W75049	me52h08.r1
AZ470048	1M0283L20
AZ809396	2M0073E21
CG571160	FTE000293
Z19901	HSAAAZAM P
BH906540	SALK_0338
CG885346	SALK_1469
CF652273	45-L02016
AI873248	wf41d06.x
AG189240	Pan trogl
CG031050	104_259_1
AW420201	fj88f06.y
BO756208	EBem05 SO
CR359149	Arabidops
AZ964660	2M0234M21
AV952014	W952014
CL211120	W191D04 G
BX763192	BX763192
AJ747306	AT747306
CZ490547	f07803-3p
CZ490549	f07804-3p
DR038246	BNE000002
BQ586352	F012395-0
CR147982	Forward s
CG509165	OSF60111
AL755545	Arabidops
BZ290183	SALK_0236
BZ290481	SALK_0239
BH847153	SALK_0135

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97 11.4 63.3 77 10 CG490588
98 11.4 63.3 79 9 BH906286
c 99 11.4 63.3 80 3 BM098397
c 100 11.2 62.2 42 10 CZ476761

ALIGNMENTS

CC556903 72 bp DNA GSS 18-JUN-2003
CH240_464F22.T7 CHORI-240 Bos taurus genomic clone CH240_464F22,
genomic survey sequence.
ACCESSION CC556903
VERSION CC556903.1 GI:31884266
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 72)
Holt.R., Stott.J., Yang.G., Barber.S., Smalilus.D., Prabhu.A.-L.,
Tsai.M., Cloutier.A., Lee.D., Ginn.N., Olson.T., Mayo.M., Chiu.R.,
Butterfield.Y., Kirkpatrick.R., Liu.J., Guin.R., Chan.A., Chiu.R.,
Mathewson.C., Wye.N., Masson.A., Brown-John.M., Jones.S.,
Schein.J., Marra.M., de Jong.P., Keele.J.W. and Kappes.S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
JOURNAL Unpublished (2003)
COMMENT Other GSSs: CH240_464F22.TARBAC13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bccsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 464 row: F column: 22
Seq primer: T7
Class: BAC ends.
FEATURES
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    /organism="Bos taurus"
    /mol_type="genomic DNA"
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    /db_xref="taxon:9913"
    /clone="CH240_464F22"
    /sex="Male"
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    /clone_lib="CHORI-240"
    /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
    Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
    library (Male) produced by Pieter de Jong"

Query Match 82.2%; Score 14.8; DB 9; Length 72;
Best Local Similarity 88.9%; Pred. No. 6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
    ||| ||||| ||||| |||
Db 11 CATAAAGTGGCCGAGA 28

RESULT 1
LOCUS CC556903
DEFINITION CH240_464F22.T7 CHORI-240 Bos taurus genomic clone CH240_464F22,
genomic survey sequence.
ACCESSION CC556903
VERSION CC556903.1 GI:31884266
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 72)
Holt.R., Stott.J., Yang.G., Barber.S., Smalilus.D., Prabhu.A.-L.,
Tsai.M., Cloutier.A., Lee.D., Ginn.N., Olson.T., Mayo.M., Chiu.R.,
Butterfield.Y., Kirkpatrick.R., Liu.J., Guin.R., Chan.A., Chiu.R.,
Mathewson.C., Wye.N., Masson.A., Brown-John.M., Jones.S.,
Schein.J., Marra.M., de Jong.P., Keele.J.W. and Kappes.S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
JOURNAL Unpublished (2003)
COMMENT Other GSSs: CH240_464F22.TARBAC13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bccsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 464 row: F column: 22
Seq primer: T7
Class: BAC ends.
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    /organism="Bos taurus"
    /mol_type="genomic DNA"
    /strain="breed: Hereford"
    /db_xref="taxon:9913"
    /clone="CH240_464F22"
    /sex="Male"
    /cell_type="Blood"
    /clone_lib="CHORI-240"
    /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
    Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
    library (Male) produced by Pieter de Jong"

Query Match 82.2%; Score 14.8; DB 9; Length 72;
Best Local Similarity 88.9%; Pred. No. 6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
    ||| ||||| ||||| |||
Db 11 CATAAAGTGGCCGAGA 28

RESULT 2
LOCUS BM434781
DEFINITION BM434781 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION BM434781
VERSION BM434781.1 GI:18456503
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 58)
Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W.,
Gordon,P.M.K. and Moore,S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 58 Std Error: 0.00
POLYA=No.
FEATURES
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    1..58
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    /mol_type="mRNA"
    /db_xref="taxon:9913"
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    /lab_host="XL1-BlueMRF'st strain"
    /clone_lib="Bos taurus Reticulum #1 library"
    /note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site_1:
    EcoRI; Site_2: Xho I"

Query Match 76.7%; Score 13.8; DB 3; Length 58;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAGA 18
    ||| ||||| ||||| |||
Db 6 ATCAAGGTGGCCGAGA 22

RESULT 3
LOCUS CL982875/c
DEFINITION CL982875 TIGEM gene trap library Mus musculus cDNA clone 8322.18,
mRNA sequence.
ACCESSION CL982875
VERSION CL982875.1 GI:52420237
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 43)
Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,
Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
Contact: TIGEM
107

```

TIGEM  
Via P. Castellino, 111, 80131 NAPOLI, ITALY  
Tel: +390816132205  
Fax: +390815790919  
Email: cobellis@tigem.it  
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM  
Class: Gene Trap.

FEATURES	source	Location/Qualifiers
	1. .43	
		/organism="Mus musculus"
		/mol_type="mRNA"
		/strain="129 Ola"
		/db_xref="taxon:10090"
		/clone="8322.18"
		/sex="male"
		/cell_type="Embryonic stem cell"
		/cell_line="E14"
		/clone_lib="TIGEM gene trap library"
		/note="Vector: pF1p1"

## ORIGIN

Query Match	74.4%	Score 13.4;	DB 10;	Length 43;
Best Local Similarity	93.3%;	Pred. No. 3.1e+04;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy 4 CAAAGGTGGCCGAGA 18  
Db 38 CAAAGGTGGCCGAGA 24

RESULT 4	CG8000410	CG8000410
LOCUS	1118012A01.1EL x1 1118	
DEFINITION	survey sequence.	
ACCESSION	CG8000410	CG8000410.1
VERSION		GI:38236196
KEYWORDS	GSS.	
SOURCE	zea mays	
ORGANISM	Zea mays	

REFERENCE	1 (bases 1 to 53)
AUTHORS	Walbot, V.
TITLE	Maize genomic sequences found using engineered RescueMu transposon
JOURNAL	Unpublished (2001)
COMMENT	Contact: Walbot V

Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1118012 row: 25  
Class: transposon-tagged.

**FEATURES**  
**SOURCE**

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1. 53
/location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="1118 - RescueMu Grid S"
/notes="Organ: leaf; Vector: RescueMu (eng
pBScript backbone); Site 1: BamHI; Site

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/crom1112-1110 RescueMu Grid 5
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BclII;

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## ORIGIN

RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site '[www.zmdb.iastate.edu](http://www.zmdb.iastate.edu)' and follow the links for 'RescueMu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

```
Query Match      74.4%; Score 13.4; DB 10; Length 53;
Best Local Similarity 93.3%; Pred. No. 3.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 ATCAAAGGTGGCCGA 16  
Dp 21 ATCAAAGGTGGCCAA 35

RESULT 5  
CG726326

LOCUS	CG726326	60 bp	DNA	linear	GSS 20-OCT-2003
DEFINITION	1119089807.1EL.x1	1119	- RescueMu	Grid AA	zea mays genomic, genomic survey sequence.

ACCESSION CG726326  
VERSION CG726326.1 GI:37764970  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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1 (bases 1 to 60)  
Walbot.v.  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1119089 row: 11  
Class: transposon-tagged.

**FEATURES**  
**SOURCE**

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/organism="Zea mays"
/mol_type="genomic DNA"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmld.iastate.edu' and follow the links for 'RescueMu'. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

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Query Match      74.4%; Score 13.4; DB 10; Length 60;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAAGGTGCCGA 16
Db 16 ATCAAAGGTGCCAA 30

RESULT 6
CG806795
LOCUS
DEFINITION 1118074A04.1BL x1 1118 - RescueMu Grid S Zea mays genomic, genomic
survey sequence.
ACCESSION CG806795
VERSION CG806795
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 63)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
CONTACT: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118074 row: 1
Class: transposon-tagged.
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Location/Qualifiers
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/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
sites. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match      74.4%; Score 13.4; DB 10; Length 63;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAAGGTGCCGA 16
Db 19 ATCAAAGGTGCCAA 33

RESULT 7
CW020333/c
LOCUS

```

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DEFINITION GC0591 TIGEM gene trap library Mus musculus cDNA clone 9148.105,
mRNA sequence.
ACCESSION CW020333
VERSION CW020333.1 GI:52789593
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 69)
Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
FEATURES
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Location/Qualifiers
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/strain="129 Ola"
/db_xref="taxon:10090"
/clone="9148.105"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"

ORIGIN
Query Match      74.4%; Score 13.4; DB 10; Length 69;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAAAGGTGCCGAGA 18
Db 38 CAAAGGTGCCGAGA 24

RESULT 8
DME426975/c
LOCUS
DEFINITION Drosophila melanogaster X chromosomal sequence flanking P-lacW
insertion, strain 1(l)G0074, genomic survey sequence.
ACCESSION AJ426975
VERSION AJ426975.1 GI:18478196
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
REFERENCE Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1
Peter, A., Schottler, P., Werner, M., Beinert, N., Dowe, G., Burkert, P.,
Mourikoti, F., Denter, L., He, Y., Deak, P., Benos, P.V., Gatt, M.K.,
Murphy, L., Harris, D., Barrell, B., Ferraz, C., Vidal, S., Brun, C.,
Demaille, J., Cadieu, E., Dreano, S., Gloux, S., Lelaure, V.,
Mottier, S., Galibert, F., Borkova, D., Minana, B., Kafatos, F.C.,
Bolshakov, S., Siden-Kiamos, I., Papagiannakis, G., Spanos, L.,
Louis, C., Madueno, E., de Pablos, B., Modolell, J., Bucheton, A.,

```

Callister, D., Campbell, L., Henderson, N.S., McMillan, P.J.,  
Salles, C., Tait, E., Valenti, P., Saunders, R.D., Billaud, A.,  
Pachter, L., Klapper, R., Janning, W., Glover, D.M., Ashburner, M.,  
Bellen, H.J., Jackle, H. and Schaefer, U.  
Mapping and identification of essential gene functions on the X  
chromosome of *Drosophila*

JOURNAL ENBO Rep. 3 (1), 34-38 (2002)  
PUBMED 11751581  
REFERENCE 2 (bases 1 to 59)

AUTHORS Schaefer, U.  
TITLE Direct Submission

JOURNAL Submitted (03-DEC-2001) Schaefer U., Abt. Molekulare  
Entwicklungsbiologie, Max-Planck-Institut fuer biophysikalische  
Chemie, Am Fassberg 11, D-37077, GERMANY  
COMMENT P insertion putatively linked to X chromosomal lethality.

FEATURES Location/Qualifiers

1..59  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="1(1)G0074"  
/db\_xref="taxon:7227"  
/chromosome="X"  
/map="16D1-2"  
/note="isolated by 5' inverse PCR"

misc\_feature 52..59

/notes="8 bp target duplication after P-lacW insertion"

ORIGIN

Query Match 73.3%; Score 13.2; DB 11; Length 59;  
Best Local Similarity 83.3%; Pred. No. 4.2e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18

||||| ||||| ||||| ||||| |||||  
Db 46 CATCATCGTGGCAGAGA 29

RESULT 9  
CG802312/c

LOCUS 1118029F10.2EL\_x1 1118 - RescueMu Grid S Zea mays genomic, genomic  
DEFINITION survey sequence.

ACCESSION CG802312

VERSION CG802312.1 GI:38238098

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 61)

Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)

CONTACT Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1118029 row: 5

Class: transposon-tagged.

Location/Qualifiers

FEATURES

source

1..61  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"

/lab\_host="DH10B"  
/clone\_lib="1118 - RescueMu Grid S"  
/notes="Organ: leaf; Vector: RescueMu (engineered from  
pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
RescueMu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on RescueMu, go to the web  
site 'www.zmdb.iastate.edu' and follow the links for  
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was  
extracted from leaf strips, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

ORIGIN

Query Match 73.3%; Score 13.2; DB 10; Length 61;  
Best Local Similarity 83.3%; Pred. No. 4.2e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18

||||| ||||| ||||| ||||| |||||

Db 42 CATCAATGGCGCCGAGA 25

RESULT 10

AZ339975/c

LOCUS

DEFINITION 1M0071N10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0071N10 R, genomic survey sequence.

ACCESSION AZ339975

VERSION AZ339975.1 GI:10414777

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 53)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0071 row: N column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 53.

FEATURES

Location/Qualifiers

source

1..53  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0071N10"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 71.1%; Score 12.8; DB 9; Length 53;  
Best Local Similarity 87.5%; Pred. No. 6.7e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17  
|||||||  
Db 46 ATCAAGGTGCCGAG 31

## RESULT 11

AA646597/c  
LOCUS  
DEFINITION  
64 bp mRNA linear EST 28-OCT-1997  
v646e05.r1 Soares mammary gland NbMMG Mus musculus cDNA clone  
IMAGE:821216 5' similar to TR:G677916 G677916 UBIQUITIN PROTEASE.  
; mRNA sequence.

## ACCESSION

AA646597  
VERSION  
AA646597.1 GI:2573026

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Mus.  
1 (bases 1 to 64)  
Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, F., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

## TITLE

The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:489496

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 1.

## FEATURES

source  
1. .64  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:821216"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"

## ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 64;  
Best Local Similarity 87.5%; Pred. No. 6.9e+04;

/clone lib="Soares mammary gland NbMMG"  
/note="Organ: mammary gland; Vector: p7T3D-Pac  
(Pharmacia) with a modified polylinker; Site 1: Not I;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCGCAATGGTGTCTTTTTTTTTTTTTTTT  
T 3'] double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified p7T3 vector.  
RNA provided by Dr. Minoru KO, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M.Fatima  
Bonaldo."

## ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 64;  
Best Local Similarity 87.5%; Pred. No. 6.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCAAGGTGCCGAGA 18  
|||||||  
Db 57 TCAAGGTGCCGAGA 42

## RESULT 12

AI624617/c  
LOCUS  
DEFINITION  
64 bp mRNA linear EST 22-APR-1999  
t669b07.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:2233813 3'  
similar to TR:Q16540 Q16540 L23-RELATED PROTEIN. ;contains element  
MER26 repetitive element ;, mRNA sequence.

## ACCESSION

AI624617

## VERSION

AI624617.1 GI:4649548

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 64)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Greg Lennon, Ph.D.  
CDNA Library Arrayed by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

## FEATURES

source  
1. .64  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2233813"  
/tissue\_type="renal cell tumor"  
/lab\_host="DH10B"  
/clone lib="NCI CGAP Kid8"  
/note="Organ: kidney; Vector: pCWM-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.2 kb. Life Technologies catalog #:  
11524-014"

```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATCAAGGTGGCCGAG 17
    |||||
DB 38 ATCAAGGTGGCCAG 23

RESULT 13
AZ621111
LOCUS 78 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0454E08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454E08 F, genomic survey sequence.
ACCESSION AZ621111
VERSION 1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 78)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: E column: 08
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 78.
FEATURES
Location/Qualifiers
1..78
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0454E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 71.1%; Score 12.8; DB 9; Length 78;

```

```

Best Local Similarity 87.5%; Pred. No. 7.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 TCACAGGTGGCCGAGA 18
    |||||
DB 21 TCACAGGTGGCTGAGA 36

RESULT 14
BJ016067
LOCUS 45 bp mRNA linear EST 05-DEC-2001
DEFINITION BJ016067 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA008F01 3',
mRNA sequence.
ACCESSION BJ016067
VERSION 1
KEYWORDS EST.
SOURCE Oryzias latipes (Japanese medaka)
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 45)
Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..45
/organism="Oryzias latipes"
/mol_type="mRNA"
/strain="Hg-r"
/db_xref="taxon:8090"
/clone="MF01SSA008F01"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
/clone_lib="MF01SSA cDNA"
ORIGIN
Query Match 68.9%; Score 12.4; DB 3; Length 45;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CATCAAGGTGGCC 14
    |||||
DB 27 CATCTAAGGTGGCC 40

RESULT 15
AV834194
LOCUS 57 bp mRNA linear EST 09-MAY-2002
DEFINITION AV834194 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
clone bag66915, mRNA sequence.
ACCESSION AV834194
VERSION 1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 57)
Sato,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)

```

```

COMMENT
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL: http://www.rib.okayama-u.ac.jp/barley/
database: http://www.shigen.nig.ac.jp/barley/barley.html.

FEATURES
    source
        1..57
            /organism="Hordeum vulgare subsp. vulgare"
            /mol_type="mRNA"
            /cultivar="Haruna Nijo"
            /sub_species="vulgare"
            /db_xref="taxon:112509"
            /clone="bags613"
            /tissue_type="shoots"
            /dev_stage="germination"
            /clone_lib="K. Sato unpublished cDNA library: Hordeum
            vulgare subsp. vulgare shoots germination"

ORIGIN
Query Match      68.9%; Score 12.4; DB 1; Length 57;
Best Local Similarity 86.7%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCAAAGTGGCCGAG 17
    |||||
Db 46 TCAAAGGTGACGAG 32

RESULT 16
CG591414
LOCUS
DEFINITION
OST245945 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST245945,
mRNA sequence.
ACCESSION
CG591414
VERSION
CG591414.1 GI:37399301
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 67)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
    1..67
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="129Sv/Ev"
        /db_xref="taxon:10090"
        /clone="OST245945"
        /cell_type="embryonic stem cell"
        /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match      68.9%; Score 12.4; DB 1; Length 71;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAG 17
    |||||
Db 27 CAAAGGTGCACAG 40

RESULT 17
AW164603
LOCUS
DEFINITION
se74a07.y1 Gm-cl023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl023-397 5', mRNA sequence.
ACCESSION
AW164603
VERSION
AW164603.1 GI:6341717
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 71)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvelli, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Other ESTs: B822937 corresponding to Gm-r1070-7396 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57066 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 51.
Location/Qualifiers
    1..71
        /organism="Glycine max"
        /mol_type="mRNA"
        /cultivar="rl57"
        /db_xref="taxon:3847"
        /tissue_type="seed coats of greenhouse grown plants"
        /lab_host="DH10B"
        /clone_lib="Gm-cl023"
        /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
        cDNA library was constructed from mRNA isolated from seed
        coats (100-200mgs) of greenhouse grown plants. The
        library was prepared using the Life Technologies
        SuperScript cDNA library construction kit. Complementary
        DNA was synthesized from mRNA using a poly (dT) sequence
        with a Not I restriction site. Sal I linkers adapers
        were ligated to the blunt-ended cDNA fragments followed by
        Not I digestion. The cDNA fragments were directionally
        cloned into the Not I-Sal I restriction site of the
        pSPORT1 vector. The ligated cDNA fragments were
        transformed into E.coli: Electromax DH10B host cells. This
        library was constructed by Dr. Lila Vodkin and Dr. Anu
        Khanna."

ORIGIN
Query Match      68.9%; Score 12.4; DB 1; Length 71;

```



```

Best Local Similarity 92.9%; Pred. No. 1.1e+05; Mismatches 1; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 19 CAAAGGTGGCCGAG 32
    |||||

RESULT 18
CG514254 74 bp mRNA linear GSS 01-OCT-2003
OST67986 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST67986,
mRNA sequence.
CG514254
CG514254.1 GI:37300827
Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 74)
REFERENCE
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
LOCATION/Qualifiers
1..74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST67986"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 68.9%; Score 12.4; DB 10; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 37 CAAAGGTGGCCGAG 50
    |||||

RESULT 19
CG510224 77 bp mRNA linear GSS 01-OCT-2003
OST61835 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST61835,
mRNA sequence.
CG510224
CG510224.1 GI:37294274
Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 77)
REFERENCE
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
LOCATION/Qualifiers
1..74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST67986"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 68.9%; Score 12.4; DB 10; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 37 CAAAGGTGGCCGAG 50
    |||||

RESULT 20
BPI33993/3 79 bp mRNA linear EST 05-NOV-2004
MAT001 Nicotiana tabacum cDNA clone BVE321, mRNA sequence.
BPI33993
BPI33993.1 GI:32876878
Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 79)
REFERENCE
AUTHORS Matsuo,K., Demura,T., Galis,I., Horiguchi,T., Sasaki,M.,
Tashiro,G. and Fukuda,H.
A Comprehensive Gene Expression Analysis Toward the Understanding
of Growth and Differentiation of Tobacco BY-2 Cells
Plant Cell Physiol. 45 (9), 1280-1289 (2004)
15509851
CONTACT: Ken Matsuo
Morphogenesis Research Group
RIKEN Plant Science Center
1-7-2 Suehirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
Email: by2@psc.riken.go.jp, URL:http://mrq.psc.riken.go.jp/strc/
The cDNA library was constructed from mRNA isolated from lag (9 h),
log (72 h) and stationary (7 days) old BY-2 cells.
FEATURES
source
LOCATION/Qualifiers
1..79
/organism="Nicotiana tabacum"
/mol_type="mRNA"

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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 77)
REFERENCE
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
LOCATION/Qualifiers
1..77
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST61835"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 68.9%; Score 12.4; DB 10; Length 77;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 38 CAAAGGTGGCCGAG 51
    |||||

RESULT 20
BPI33993/3 79 bp mRNA linear EST 05-NOV-2004
MAT001 Nicotiana tabacum cDNA clone BVE321, mRNA sequence.
BPI33993
BPI33993.1 GI:32876878
Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 79)
REFERENCE
AUTHORS Matsuo,K., Demura,T., Galis,I., Horiguchi,T., Sasaki,M.,
Tashiro,G. and Fukuda,H.
A Comprehensive Gene Expression Analysis Toward the Understanding
of Growth and Differentiation of Tobacco BY-2 Cells
Plant Cell Physiol. 45 (9), 1280-1289 (2004)
15509851
CONTACT: Ken Matsuo
Morphogenesis Research Group
RIKEN Plant Science Center
1-7-2 Suehirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
Email: by2@psc.riken.go.jp, URL:http://mrq.psc.riken.go.jp/strc/
The cDNA library was constructed from mRNA isolated from lag (9 h),
log (72 h) and stationary (7 days) old BY-2 cells.
FEATURES
source
LOCATION/Qualifiers
1..79
/organism="Nicotiana tabacum"
/mol_type="mRNA"

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/cultivar="Bright Yellow No.2"
/db xref="taxon:4097"
/clone="BY6321"
/cell_line="BY-2"
/clone_lib="WAT001"
/note="Vector: pGEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"

ORIGIN
Query Match      68.9%; Score 12.4; DB 3; Length 79;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAAGGTGGCCGAGA 18
    ||||| |||||
Db 45 AAAGGTAGCCGAGA 32

RESULT 21
CZ487115/c
LOCUS      CZ487115          29 bp      DNA      linear      GSS 29-APR-2005
DEFINITION f04573-3prime Exelixis piggyBac WH insertions Drosophila
            melanogaster genomic Sequence recovered from 5' end of piggyBac,
            genomic survey sequence.
ACCESSION  CZ487115
VERSION     CZ487115.1 GI:62984553
KEYWORDS   GSS.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
REFERENCE  1 (bases 1 to 29)
AUTHORS    Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
            Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
            Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
            Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
            Laufer,A., Mazrotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
            Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
            Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
TITLE      A complementary transposon tool kit for Drosophila melanogaster
JOURNAL    Nat. Genet. 36 (3), 283-287 (2004)
PUBMED    14981521
COMMENT    Contact: Roger A Hoskins
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory
            Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
            Tel: 510 486 4015
            Fax: 510 486 6798
            Email: Rhoskins@lbl.gov
            Sequence recovery method was inverse PCR.
            Sequence orientation is forward strand relative to 5' end of
            piggyBac element.
            The piggyBac insertion position is 26 in the 29 bases. This
            insertion position refers to the first base of the 4 base TTAA
            target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1..29
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db strain="isogenic w- strain"
/db xref="taxon:7227"
/clone_lib="Exelixis piggyBac WH insertions"
/note="Vector: piggyBac WH (GenBank accession number
AV515148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin:piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsincy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

ORIGIN
Query Match      67.8%; Score 12.2; DB 10; Length 29;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18
    ||||| |||||
Db 19 ACCAATGGTGGCCGAGA 3

RESULT 22
BH850478
LOCUS      BH850478          31 bp      DNA      linear      GSS 13-JUN-2002
DEFINITION SALK_071331.38.75.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_071331.38.75.x, genomic
            survey sequence.
ACCESSION  BH850478
VERSION     BH850478.1 GI:21421349
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 31)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,W., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL    Unpublished (2001)
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..31
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db xref="taxon:3702"
/clone="SALK_071331.38.75.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      67.8%; Score 12.2; DB 9; Length 31;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
    ||||| |||||
Db 1 CATCAACCGTGGCCGAG 17

RESULT 23

```

CZ483104/c  
LOCUS  
DEFINITION  
F00637-5prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic sequence recovered from 5' end of piggyBac, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CZ483104.1 GI:62980542  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 56)  
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.  
A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac  
Nat. Genet. 36 (3), 283-287 (2004)  
14981521  
Contact: Roger A Hoskins  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015  
Fax: 510 486 6798  
Email: RHoskins@lbl.gov  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of piggyBac element.  
The piggyBac insertion position is 53 in the 56 bases. This insertion position refers to the first base of the 4 base TTAAG target recognition sequence.  
Class: transposon insertion site.  
Location/Qualifiers  
1..56  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="isogenic w- strain"  
/db\_xref="taxon:7227"  
/clone\_lib="Exelixis piggyBac WH insertions"  
/note="Vector: piggyBac WH (GenBank accession number AF15148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin:piggyBac transposase source. We remobilized the WH element from a single amnionium element on the Binsincy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN  
Query Match 67.8%; Score 12.2; DB 10; Length 56;  
Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CATCAAGGTGGCCGAG 17  
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Db 26 CATCAAGGTGGTCGAG 10  
||||| |||||  
RESULT 24  
BG409364/c  
LOCUS  
59 bp mRNA linear EST 13-MAR-2001  
BG409364

gb91e01.y1 Moss EST library PPG Physcomitrella patens cDNA clone  
PEP SOURCE ID: PPG CopyA-130902 5', mRNA sequence.  
BG409364  
EST.  
BG409364.1 GI:13315709  
Physcomitrella patens  
Physcomitrella patens  
Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.  
1 (bases 1 to 59)  
Quatrano, R., Bashardes, S., Cove, D., Cumming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.  
Leeds/Wash U Moss EST Project  
Unpublished (1999)  
Contact: Ralph Quatrano  
Leeds/Wash U Moss EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Libraries were constructed by Dr. Stavros Bashardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)  
Putative full length read  
vector to vector length is 60  
Seq primer: -40RP from Gibco.  
Location/Qualifiers  
1..59  
/organism="Physcomitrella patens"  
/mol\_type="mRNA"  
/db\_xref="taxon:3218"  
/clone="PEP SOURCE ID: PPG CopyA-130902"  
/tissue="gametophore: 30 day old tissue, ammonium-grown"  
/lab\_host="DH10B"  
/clone\_lib="Moss EST library PPG"  
/note="Vector: pAMP1; Construction of the cDNA library was performed by Dr. W. Gregg Clark using a modification of the cDNA synthesis protocol developed in the laboratory of Dr. Michael Lovett by Dr. Yulia Korshunova (personal communication). First polyA + RNA was isolated from total gametophore RNA using oligo dT magnetic beads. Following this, first strand cDNA synthesis was performed on the bead-bound polyA + RNA, during which an oligonucleotide anchor sequence was incorporated onto the 5'-ends of the cDNA. PCR amplification was then used to synthesize the second strand, to amplify the double stranded DNA, and to incorporate dUTP containing sequences into the ends of the double stranded cDNA. This DNA was size selected and cloned into pAMP1 using the CloneAMP pAMP1 System (Life Technologies, GibcoBRL) for cloning amplification products by a non-restriction site dependant process. The cloning was directional based on sequence asymmetry introduced at the ends during PCR amplification. The 3' cDNA ends are proximal to the NotI site of the multiple cloning site in pAMP1. This annealing mixture was transformed into chemically competent DH10B cells and selected for ampicillin resistant growth. The resulting clones (about 330,000) were pooled to make the library."

ORIGIN  
Query Match 67.8%; Score 12.2; DB 2; Length 59;  
Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CATCAAGGTGGCCGAG 17  
||||| |||||

Db 44 CCTCAAAGATGCCGCGTG 28

RESULT 25  
CG575872/c  
LOCUS  
DEFINITION CG575872 63 bp mRNA linear GSS 02-OCT-2003  
OST210072 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST210072,  
mRNA sequence.  
ACCESSION CG575872  
VERSION CG575872.1 GI:37366209  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 63)  
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.  
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED 14610273  
COMMENT Contact: Zambrowicz BP  
OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.  
FEATURES  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST210072"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"  
ORIGIN  
Query Match 67.8%; Score 12.2; DB 10; Length 63;  
Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 CATCAAAGTGCGCGAG 17  
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Db 17 CATGAAAGGGGCGCGC 1  
Search completed: March 3, 2006, 11:01:24  
Job time : 990.737 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds  
(without alignments)  
2714.499 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 ctgtctagaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.8	76.7	65	6	CQ557748 Sequence
2	13.4	74.4	20	6	AX298577 Sequence
3	13.4	74.4	30	6	AX528800 Sequence
4	13.4	74.4	60	6	CQ547222 Sequence
5	13.2	73.3	37	6	BD181212 Sequence
6	13.2	73.3	37	6	AX522090 Sequence
7	13.2	73.3	53	6	I32831 Sequence 13
8	13.2	73.3	60	6	CQ538595 Sequence
9	13.2	73.3	60	6	CQ543182 Sequence
10	13.2	73.3	62	6	I32833 Sequence 15
11	13.2	73.3	65	6	AX083959 Sequence
12	13.2	73.3	65	6	CQ557381 Sequence
13	13.2	73.3	65	6	CQ559197 Sequence
14	13	72.2	70	6	E14578 DNA encodin
15	13	72.2	70	6	E14579 DNA encodin
16	12.8	71.1	17	6	AX273086 Sequence
17	12.8	71.1	18	6	BD104284 Kit and m
18	12.8	71.1	18	6	BD104285 Kit and m

BD106033 Novel LDL	20	6	BD106033	71.1	20	6	BD106033
AR305122 Sequence	20	6	AR305122	71.1	20	6	AR305122
AR309226 Sequence	20	6	AR309226	71.1	20	6	AR309226
BD251172 Functiona	23	6	BD251172	71.1	23	6	BD251172
AX712114 Sequence	28	6	AX712114	71.1	28	6	AX712114
AR489327 Sequence	38	6	AR489327	71.1	38	6	AR489327
CQ007942 Sequence	51	6	CQ007942	71.1	51	6	CQ007942
AX117897 Sequence	51	6	AX117897	71.1	51	6	AX117897
CQ542693 Sequence	60	6	CQ542693	71.1	60	6	CQ542693
CQ548019 Sequence	60	6	CQ548019	71.1	60	6	CQ548019
CQ550743 Sequence	60	6	CQ550743	71.1	60	6	CQ550743
AX391527 Sequence	15	6	AX391527	68.9	15	6	AX391527
CQ801000 Sequence	27	6	CQ801000	68.9	27	6	CQ801000
AR288675 Sequence	47	6	AR288675	68.9	47	6	AR288675
CQ003044 Sequence	51	6	CQ003044	68.9	51	6	CQ003044
AX613045 Sequence	50	6	AX613045	67.8	50	6	AX613045
AX613043 Sequence	50	6	AX613043	67.8	50	6	AX613043
AX613046 Sequence	50	6	AX613046	67.8	50	6	AX613046
CQ536228 Sequence	60	6	CQ536228	67.8	60	6	CQ536228
CQ548094 Sequence	60	6	CQ548094	67.8	60	6	CQ548094
CQ549114 Sequence	60	6	CQ549114	67.8	60	6	CQ549114
CQ562630 Sequence	60	6	CQ562630	67.8	60	6	CQ562630
AR126060 Sequence	62	6	AR126060	67.8	62	6	AR126060
CQ532194 Sequence	65	6	CQ532194	67.8	65	6	CQ532194
CQ556366 Sequence	65	6	CQ556366	67.8	65	6	CQ556366
CQ557526 Sequence	65	6	CQ557526	67.8	65	6	CQ557526
AR055468 Sequence	22	6	AR055468	66.7	22	6	AR055468
AX600785 Sequence	22	6	AX600785	66.7	22	6	AX600785
AR138974 Sequence	30	6	AR138974	66.7	30	6	AR138974
I44864 Sequence 4	30	6	I44864	66.7	30	6	I44864
AR208296 Sequence	30	6	AR208296	66.7	30	6	AR208296
CQ760652 Sequence	39	6	CQ760652	66.7	39	6	CQ760652
I83409 Sequence 10	40	6	I83409	66.7	40	6	I83409
CQ537842 Sequence	60	6	CQ537842	66.7	60	6	CQ537842
CQ539418 Sequence	60	6	CQ539418	66.7	60	6	CQ539418
AX486602 Sequence	65	6	AX486602	66.7	65	6	AX486602
AR329566 Sequence	16	6	AR329566	65.6	16	6	AR329566
AR188262 Sequence	17	6	AR188262	65.6	17	6	AR188262
AR324115 Sequence	17	6	AR324115	65.6	17	6	AR324115
AR328730 Sequence	17	6	AR328730	65.6	17	6	AR328730
AX597575 Sequence	17	6	AX597575	65.6	17	6	AX597575
AX273327 Sequence	17	6	AX273327	65.6	17	6	AX273327
CQ840020 Sequence	20	6	CQ840020	65.6	20	6	CQ840020
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AX528497 Sequence	24	6	AX528497	65.6	24	6	AX528497
BD136232 NOVEL gen	27	6	BD136232	65.6	27	6	BD136232
AR264642 Sequence	27	6	AR264642	65.6	27	6	AR264642
AR474926 Sequence	28	6	AR474926	65.6	28	6	AR474926
AX567958 Sequence	28	6	AX567958	65.6	28	6	AX567958
AX555702 Sequence	28	6	AX555702	65.6	28	6	AX555702
AX698702 Sequence	28	6	AX698702	65.6	28	6	AX698702
AX339255 Sequence	29	6	AX339255	65.6	29	6	AX339255
AR011115 Sequence	30	6	AR011115	65.6	30	6	AR011115
AR038274 Sequence	30	6	AR038274	65.6	30	6	AR038274
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AR075204 Sequence	30	6	AR075204	65.6	30	6	AR075204
AR152616 Sequence	30	6	AR152616	65.6	30	6	AR152616
I58563 Sequence 28	30	6	I58563	65.6	30	6	I58563
I61228 Sequence 35	30	6	I61228	65.6	30	6	I61228
I86667 Sequence 7	30	6	I86667	65.6	30	6	I86667
AR219325 Sequence	30	6	AR219325	65.6	30	6	AR219325
AR238456 Sequence	30	6	AR238456	65.6	30	6	AR238456
AR367618 Sequence	30	6	AR367618	65.6	30	6	AR367618
AR455480 Sequence	30	6	AR455480	65.6	30	6	AR455480

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 93 11.8 65.6 33 6 AX061516 Sequence  
 94 11.8 65.6 34 6 BD218022 Sequence  
 95 11.8 65.6 34 6 AR274248 Sequence  
 96 11.8 65.6 38 6 BD140801 Monitorin  
 97 11.8 65.6 38 6 BD140952 Monitorin  
 98 11.8 65.6 42 6 AR126195 Sequence  
 99 11.8 65.6 42 6 AR126196 Sequence  
 100 11.8 65.6 42 6 AR126197 Sequence

## ALIGNMENTS

RESULT 1  
 CQ557748  
 LOCUS AX323297 65 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 27383 from Patent WO0210449.  
 ACCESSION CQ557748  
 VERSION CQ557748.1 GI:41524175  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
 AUTHORS Oligonucleotide library for detecting rna transcripts and splice  
 TITLE variants that populate a transcriptome  
 JOURNAL Patent: WO 0210449-A 27383 07-FEB-2002;  
 CompuGen Inc. (US)  
 FEATURES Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:10090"

## ORIGIN

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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17  
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 Db 18 CTGCTTAGCACTGCCCA 34

RESULT 2  
 AX298577  
 LOCUS AX298577 20 bp DNA linear PAT 26-NOV-2001  
 DEFINITION Sequence 211 from Patent WO0183749.  
 ACCESSION AX298577  
 VERSION AX298577.1 GI:17128567  
 KEYWORDS  
 SOURCE Mus sp.  
 ORGANISM Mus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1 Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,  
 AUTHORS Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.  
 TITLE Gene and sequence variation associated with sensing carbohydrate  
 compounds and other sweeteners  
 JOURNAL Patent: WO 0183749-A 211 08-NOV-2001;  
 WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center  
 (US)  
 FEATURES Location/Qualifiers  
 source 1..20  
 /organism="Mus sp."  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:10095"

## ORIGIN

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Qy 1 CTGCTAGAACTGCC 15  
 |||||  
 Db 4 CTGCTAGAACTGCC 18

## RESULT 3

AX528800  
 LOCUS AX528800 30 bp DNA linear PAT 21-NOV-2002  
 DEFINITION Sequence 49 from Patent WO02059357.  
 ACCESSION AX528800  
 VERSION AX528800.1 GI:25172855  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1 Pedersen,M.L.  
 AUTHORS Assay and kit for analyzing gene expression  
 TITLE Patent: WO 02059357-A 49 01-AUG-2002;  
 JOURNAL Location/Qualifiers  
 FEATURES source 1..30  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="synthetic construct"

## ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 30;  
 Best Local Similarity 93.3%; Pred. No. 8.2e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCCAAG 18  
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 Db 3 TCTAGAACTGCCCAAG 17

## RESULT 4

CQ547222/c  
 LOCUS CQ547222 60 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 16857 from Patent WO0210449.  
 ACCESSION CQ547222  
 VERSION CQ547222.1 GI:41513486  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
 AUTHORS Oligonucleotide library for detecting rna transcripts and splice  
 TITLE variants that populate a transcriptome  
 JOURNAL Patent: WO 0210449-A 16857 07-FEB-2002;  
 CompuGen Inc. (US)  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 60;  
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Qy 4 TCTAGAACTGCCCAAG 18  
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Db      16 TCTAGAACTGTCAC 2
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LOCUS   BD181212
DEFINITION Expression-regulatory sequence.
ACCESSION BD181212
VERSION   BD181212.1 GI:30792130
KEYWORDS JP 2002320495-A/12.
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 37)
AUTHORS Mashko,S.V. and Zimenkov,D.V.
TITLE Expression-regulatory sequence
JOURNAL Patent: JP 2002320495-A 12 05-NOV-2002;
COMMENT AJINOMOTO CO INC
OS Artificial Sequence
PN JP 2002320495-A/12
PD 05-NOV-2002
PF 22-FEB-2002 JP 2002046910
PR 22-FEB-2001 RU 2001104817
PI SERGEI VLADIMIROVICH MASHKO, DANILA VADIMOVICH ZIMENKOV PC
C12N15/09,C12N9/10//C12N1/21,C12R1/19,C12N15/00 CC
Primer
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FT /organism='Artificial Sequence'.
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCTAGAACTGTCAC 18
Db 4 CTGCTAGAACTGTCAC 21
RESULT 6
AX522090
LOCUS AX522090
DEFINITION Sequence 12 from Patent EP1234883.
ACCESSION AX522090
VERSION AX522090.1 GI:24410975
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mashko,S.V. and Zimenkov,D.V.
TITLE Expression control sequence
JOURNAL Patent: EP 1234883-A 12 28-AUG-2002;
COMMENT Ajinomoto Co., Inc. (JP)
FEATURES
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/mol_type='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/notes='primer'
ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCTAGAACTGTCAC 18
Db 4 CTGCTAGAACTGTCAC 21
RESULT 7
LOCUS I32831
DEFINITION Sequence 13 from patent US 5589364.
ACCESSION I32831
VERSION I32831.1 GI:1823622
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS Williams,J.I., Pierce,J.C., Anderson,G.Mark. and Kari,P.
TITLE Recombinant production of biologically active peptides and proteins
JOURNAL Patent: US 5589364-A 13 31-DEC-1996;
COMMENT Location/Qualifiers
FEATURES
source 1..53
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCTAGAACTGTCAC 18
Db 15 CTGCTAGAACTGTCAC 32
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LOCUS CQ538595
DEFINITION Sequence 8230 from Patent WO0210449.
ACCESSION CQ538595
VERSION CQ538595.1 GI:41504859
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8230 07-FEB-2002;
COMMENT Compugen Inc. (US)
FEATURES
source 1..60
/mol_type='unassigned DNA'
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 9 CTGCTAGAACTGTCAC 26
RESULT 9
CQ543182/c
LOCUS CQ543182/c
DEFINITION Sequence 12817 from Patent WO0210449.
ACCESSION CQ543182
VERSION CQ543182.1 GI:41509446
FEATURES
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/db_xref='taxon:9606'
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCTAGAACTGTCAC 18
Db 9 CTGCTAGAACTGTCAC 26
RESULT 10
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LOCUS CQ543182/c
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ACCESSION CQ543182
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 9 CTGCTAGAACTGTCAC 26
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 12817 07-FEB-2002;
Compugen Inc. (US)
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 34 CTGTCTTGAAGTGTTCAG 17
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I32833/c
LOCUS I32833
DEFINITION Sequence 15 from patent US 5589364.
ACCESSION I32833
VERSION I32833.1 GI:1823624
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Williams,J.I., Pierce,J.C., Anderson,G.Mark. and Kari,P.
TITLE Recombinant production of biologically active peptides and proteins
JOURNAL Patent: US 5589364-A 15 31-DEC-1996;
FEATURES
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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AX083959/c
LOCUS AX083959
DEFINITION Sequence 10 from Patent WO0112658.
ACCESSION AX083959
VERSION AX083959.1 GI:13185510
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Davis,S.
TITLE Human icos ligand and application thereof
JOURNAL Patent: WO 0112658-A 10 22-FEB-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
Location/Qualifiers
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/db_xref="taxon:10090"
us-10-655-801-20.max.rge
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RESULT 12
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LOCUS CQ557381
DEFINITION Sequence 27016 from Patent WO0210449.
ACCESSION CQ557381
VERSION CQ557381.1 GI:41523808
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 27016 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source
1. .65
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 13
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LOCUS CQ559197
DEFINITION Sequence 28832 from Patent WO0210449.
ACCESSION CQ559197
VERSION CQ559197.1 GI:41525624
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 28832 07-FEB-2002;
Compugen Inc. (US)
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## ORIGIN

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 Db 2 CTGTCAGAAATGCTCAG 19

## RESULT 14

E14578  
 LOCUS DNA encoding repeat unit of artificial protein polymer. PAT 28-JUL-1999  
 DEFINITION  
 E14578  
 ACCESSION  
 E14578  
 VERSION  
 E14578.1 GI:5709261  
 KEYWORDS  
 JP 1997323999-A/3.  
 SOURCE  
 ORGANISM  
 unclassified.  
 1 (bases 1 to 70)  
 FUKUSHIMA, Y.  
 ARTIFICIAL PROTEIN POLYMER  
 Patent: JP 1997323999-A 3 16-DEC-1997;  
 JOURNAL  
 UNITEKA LTD  
 COMMENT  
 OS None  
 OC Artificial sequences.  
 PN JP 1997323999-A/3  
 PD 16-DEC-1997  
 PF 03-JUN-1996 JP 1996139905  
 PI FUKUSHIMA YASUMASA  
 PC C07K14/435, C07H21/04, C12N1/02, (C12P21/02, (C12P21/02,  
 PC C12R1:19);  
 CC strandedness: Single;  
 CC topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1..70  
 FT /organism='Artificial sequences'.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## OS

## OC

## PN

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## PI

## PC

## CC

## CC

## FH

## FT

## FT

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## /mol\_type='genomic DNA'

## /db\_xref='taxon:32644'

## ORIGIN

## Query Match

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## Matches

## Conservative

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## 0; Indels

## 0; Gaps

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## QY

## 2

## TGCTAGAACTGC 14

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## Db

## 8

## TGCTAGAACTGC 20

## RESULT 15

## E14579/c

## LOCUS

## DNA encoding repeat unit of artificial protein polymer. PAT 28-JUL-1999

## DEFINITION

## E14579

## ACCESSION

## E14579

## VERSION

## E14579.1 GI:5709262

## KEYWORDS

## JP 1997323999-A/4.

## SOURCE

## unclassified.

## 1 (bases 1 to 70)

## FUKUSHIMA, Y.

## ARTIFICIAL PROTEIN POLYMER

Patent: JP 1997323999-A 4 16-DEC-1997;  
 JOURNAL  
 UNITEKA LTD  
 COMMENT  
 OS None  
 OC Artificial sequences.

## ORIGIN

PN JP 1997323999-A/4  
 PD 16-DEC-1997  
 PF 03-JUN-1996 JP 1996139905  
 PI FUKUSHIMA YASUMASA  
 PC C07K14/435, C07H21/04, C12N1/02, (C12P21/02, (C12P21/02,  
 PC C12R1:19);  
 CC strandedness: Single;  
 CC topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1..70  
 FT /organism='Artificial sequences'.

## FEATURES

## source

## 1..70

## /organism='unidentified'

## /mol\_type='genomic DNA'

## /db\_xref='taxon:32644'

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## 0; Mismatches

## 0; Indels

## 0; Gaps

## 0;

## QY

## 2

## TGCTAGAACTGC 14

## ||||| ||||| ||||| |||||

## Db

## 67

## TGCTAGAACTGC 55

## RESULT 16

## AX273086

## LOCUS

## Sequence 655 from Patent WO0162911.

## DEFINITION

## AX273086

## ACCESSION

## AX273086.1 GI:16545823

## KEYWORDS

## Homo sapiens (human)

## SOURCE

## Homo sapiens

## ORGANISM

## REFERENCE

## AUTHORS

## Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.

## TITLE

## Method and reagent for the inhibition of grid

## JOURNAL

Patent: WO 0162911-A 655 30-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)

## FEATURES

## source

## 1..17

## /organism='Homo sapiens'

## /mol\_type='unassigned RNA'

## /db\_xref='taxon:9606'

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

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## 2; Indels

## 0; Gaps

## 0;

## QY

## 2

## TGCTAGAACTGCCCA 17

## ||||| ||||| ||||| |||||

## Db

## 1

## TGCTGGAGCTGCCCA 16

## RESULT 17

## BD104284/c

## LOCUS

## Kit and method for determining HLA type.

## DEFINITION

## BD104284

## ACCESSION

## BD104284.1 GI:22649858

## KEYWORDS

## WO 0192572-A/388.

## SOURCE

## synthetic construct

## ORGANISM

## other sequences; artificial sequences.

## REFERENCE

## 1 (bases 1 to 18)

AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.  
 TITLE Kit and method for determining HLA type  
 JOURNAL Patent: WO 0192572-A 389 06-DEC-2001;  
 NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAeko  
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHI  
 NISHIDA  
 COMMENT OS Artificial Sequence  
 PN WO 0192572-A/389  
 PD 06-DEC-2001  
 PF 01-JUN-2001 WO 2001JP004662  
 PR 01-JUN-2000 JP OOP 164798  
 PI HIDETOSHI INOKO,TAeko KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI  
 MATSUMURA,  
 PC SHOGO MORIYA,MICHI NISHIDA  
 CC C12Q1/68,C12M1/00,C12N15/09,G01N33/53  
 CH Description of Artificial Sequence:capture  
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 FT Location/Qualifiers  
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 Best Local Similarity 87.5%; Pred.No.1.9e+04;  
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 Qy 1 CTGCTAGAACTGCC 16  
 Db 18 CTGTCAGCACTGCC 3  
 RESULT 18  
 BD104285/c  
 LOCUS 18 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Kit and method for determining HLA type.  
 ACCESSION BD104285  
 VERSION BD104285.1 GI:22649859  
 KEYWORDS WO 0192572-A/389.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 OTHER SEQUENCES; artificial sequences.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.  
 TITLE Kit and method for determining HLA type  
 JOURNAL Patent: WO 0192572-A 389 06-DEC-2001;  
 NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAeko  
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHI  
 NISHIDA  
 COMMENT OS Artificial Sequence  
 PN WO 0192572-A/389  
 PD 06-DEC-2001  
 PF 01-JUN-2001 WO 2001JP004662  
 PR 01-JUN-2000 JP OOP 164798  
 PI HIDETOSHI INOKO,TAeko KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI  
 MATSUMURA,  
 PC SHOGO MORIYA,MICHI NISHIDA  
 CC C12Q1/68,C12M1/00,C12N15/09,G01N33/53  
 CH Description of Artificial Sequence:capture  
 FH Key Location/Qualifiers  
 FT source 1..18  
 FT Location/Qualifiers  
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 Best Local Similarity 87.5%; Pred.No.1.9e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CTGCTAGAACTGCC 16  
 Db 18 CTGTCAGCACTGCC 3  
 RESULT 19  
 BD106033  
 LOCUS 20 bp DNA linear PAT 18-SEP-2002  
 DEFINITION Novel LDL-receptor.  
 ACCESSION BD106033  
 VERSION BD106033.1 GI:23200851  
 KEYWORDS JP 2002501376-A/48.  
 SOURCE Chlamydia sp.  
 ORGANISM Chlamydia sp.  
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H. and Hey,P.  
 TITLE Novel LDL-receptor  
 JOURNAL Patent: JP 2002501376-A 48 15-JAN-2002;  
 THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO  
 INC  
 COMMENT PN JP 2002501376-A/48  
 PD 15-JAN-2002  
 PF 15-APR-1998 JP 1998543635  
 PR 15-APR-1997 US 60/043553,05-JUN-1997 US 60/048740 PI  
 JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES  
 THOMAS CASKEY,ROGER  
 PI DAVID COX,  
 PI DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY  
 PC C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,  
 PC A61K39/395,  
 PC A61K48/00  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
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 Db 4 GTCTGCACTGCCAG 19  
 RESULT 20  
 AR305122  
 LOCUS 20 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 76 from patent US 6545137.  
 ACCESSION AR305122  
 VERSION AR305122.1 GI:31694432  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L., Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.  
 TITLE Receptor  
 JOURNAL Patent: US 6545137-A 76 08-APR-2003;

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    Best Local Similarity
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      14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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  Db
    4 GTCAGAACTGCCAG 19
    |||||

RESULT 21
AR309226
LOCUS
  AR309226
  Sequence 76 from patent US 655654.
  DEFINITION
    Sequence 76 from patent US 655654.
  ACCESSION
    AR309226
  VERSION
    AR309226.1 GI:31701231
  KEYWORDS
    Unknown.
  SOURCE
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 20)
    Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
    Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
    Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
  TITLE
    LDL-receptor
  JOURNAL
    Patent: US 655654-A 76 29-APR-2003;
    The Wellcome Trust Limited as Trustee for the Wellcome Trust;
    London;
    WOX;

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    Matches
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  QY
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  Db
    4 GTCAGAACTGCCAG 19
    |||||

RESULT 22
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LOCUS
  BD251172
  Functional antagonists of hedgehog activity.
  DEFINITION
    Functional antagonists of hedgehog activity.
  ACCESSION
    BD251172
  VERSION
    BD251172.1 GI:33060942
  KEYWORDS
    JP 2002534060-A/3.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominiidae; Homo.
  REFERENCE
    1 (bases 1 to 23)
    Williams, K., Rayhorn, P., Garber, E.A. and Pepinsky, B.R.
    Functional antagonists of hedgehog activity
    Patent: JP 2002534060-A 3 15-OCT-2002;
    BIOGEN INC
  COMMENT
    OS Homo sapiens (human)
    PN JP 2002534060-A/3
    PD 15-OCT-2002
    PF 02-NOV-1999 JP 2000579170
    PR 02-NOV-1998 US 60/106703
    PI KEVIN WILLIAMS, PAUL RAYHORN, ELLEN A GARBER, BLAKE R PEPINSKY PC
    C12N15/09, A61K38/00, A61P35/00, A61P43/00, C07K14/47, C07K17/08, PC
    WOX;

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    Best Local Similarity
      87.5%; Pred. No. 1.9e+04;
    Matches
      14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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    |||||
  Db
    5 GTCAGAACTGCCAG 20
    |||||

RESULT 23
AX712114/c
LOCUS
  AX712114
  Sequence 27 from Patent WO03018798.
  DEFINITION
    Sequence 27 from Patent WO03018798.
  ACCESSION
    AX712114
  VERSION
    AX712114.1 GI:29823355
  KEYWORDS
    synthetic construct
    SOURCE
    synthetic construct
    ORGANISM
    other sequences; artificial sequences.
  REFERENCE
    1
    Kaupmann, K.
    G-protein coupled receptor and dna sequences thereof
    Patent: WO 03018798-A 27 06-MAR-2003;
    Novartis AG (CH)
  TITLE
    G-protein coupled receptor and dna sequences thereof
  JOURNAL
    Patent: WO 03018798-A 27 06-MAR-2003;
    Novartis AG (CH)
  ORIGIN
    Query Match
      71.1%; Score 12.8; DB 6; Length 28;
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      87.5%; Pred. No. 1.9e+04;
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      14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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    |||||
  Db
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    |||||

RESULT 24
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LOCUS
  AR489327
  Sequence 80 from patent US 6709861.
  DEFINITION
    Sequence 80 from patent US 6709861.
  ACCESSION
    AR489327
  VERSION
    AR489327.1 GI:47256285
  KEYWORDS
    Unknown.
  SOURCE
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 38)
    Mead, D.A. and Godiska, R.
    Cloning vectors and vector components
    Patent: US 6709861-A 80 23-MAR-2004;
    Lucigen Corp.; Middleton, WI;
    WOX;

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/mol_type="genomic DNA"

ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 38;
Best Local Similarity 87.5%; Pred.No. 2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      26  GTTACAACTGCCAG 11

RESULT 25
CQ007942
LOCUS      51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 6582 from Patent WO0147944.
ACCESSION CQ007942
VERSION CQ007942.1 GI:41014618
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS      Shimkets, R.A. and Leach, M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL      Patent: WO 0147944-A 6582 05-JUL-2001;
Curagen Corporation (US)

FEATURES
source      Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/notes="Accession number cg44128902"

ORIGIN
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Best Local Similarity 87.5%; Pred.No. 2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CTGTCTAGAACTGCC 16
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Db      33  CTGTCCAGAACAGCCC 48

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Job time : 377.932 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:02:58 ; Search time 117.534 Seconds  
(without alignments)  
1020.680 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18  
Sequence: 1 ctgcttagaactgcccag 18

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	15.4	85.6	22	12	ADI13013	Adi13013 PCR prime
3	14.8	82.2	76	6	ABN51490	Abn51490 Human cdn
4	13.8	76.7	65	6	ABN54635	Abn54635 Mouse spl
5	13.4	74.4	20	6	AAS97601	Aas97601 Murine SA
6	13.4	74.4	20	12	ADM15941	Adm15941 Murine SA
7	13.4	74.4	30	6	AAD43849	Aad43849 Human HAH
8	13.4	74.4	60	6	ABN44109	Abn44109 Human spl
9	13.2	73.3	20	12	ADN58822	Adn58822 Human B7H
10	13.2	73.3	25	2	AAH88302	Aah88302 Human CD3
11	13.2	73.3	25	9	ACI78021	Act78021 Human mic
12	13.2	73.3	37	6	ABN52868	Abn52868 Plasmid p
13	13.2	73.3	50	6	ABZ04767	Abz04767 Human leu
14	13.2	73.3	50	12	ADP10075	Adp10075 50-mer ol
15	13.2	73.3	60	6	ABN35482	Abn35482 Human spl
16	13.2	73.3	60	6	ABN40069	Abn40069 Human spl
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17	4	ABL47022	71.1	23	12.8	71.1	Ab147022 Human GRI
17	11	ADM54345	71.1	24	12.8	71.1	Adm54345 Human GRI
17	14	ABE23669	71.1	25	12.8	71.1	Aeb23669 HLA-DP al
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18	6	ABL30900	71.1	27	12.8	71.1	Ab130900 Human HLA
20	2	AAV85580	71.1	28	12.8	71.1	Aav85580 LRP5 PCR
22	14	ADZ03943	71.1	29	12.8	71.1	Adz03943 Myocardia
23	3	AAA28858	71.1	30	12.8	71.1	Aaa28858 Primer 1
25	9	ACI67516	71.1	31	12.8	71.1	Act67516 Human mic
25	9	ACH57974	71.1	32	12.8	71.1	Ach57974 DNA carge
28	8	ABZ79479	71.1	33	12.8	71.1	Abz79479 Neated ge
38	6	ABQ75054	71.1	34	12.8	71.1	Abq75054 Bacteriop
51	4	AAL33374	71.1	35	12.8	71.1	Aal33374 Human SNP
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18	11	ADZ43420	68.9	42	12.4	68.9	Adz43420 PCR prime
22	2	AAV51838	68.9	43	12.4	68.9	Aav51838 Zea mays
27	2	AAQ38725	68.9	44	12.4	68.9	Aaq38725 AVP probe
27	12	ADM13058	68.9	45	12.4	68.9	Adm13058 Recombina
29	13	ADT66489	68.9	46	12.4	68.9	Adt66489 PCR prime
39	12	ADK41336	68.9	47	12.4	68.9	Adk41336 Human chr
41	2	AAV50754	68.9	48	12.4	68.9	Aav50754 Brassica
51	4	AAL28476	68.9	49	12.4	68.9	Aal28476 Human SNP
57	3	AAZ24684	68.9	50	12.4	68.9	Aaz24684 Oligonuc
57	3	AAZ29685	68.9	51	12.4	68.9	Aaz29685 T cell an
67	2	AAQ44684	68.9	52	12.4	68.9	Aaq44684 8F10-stim
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21	2	AAT84404	67.8	54	12.2	67.8	Aat84404 STM7.1 ge
21	2	AAH85563	67.8	55	12.2	67.8	Aah85563 PCR prime
22	13	ADT00687	67.8	56	12.2	67.8	Adt00687 Novel mut
25	9	ACK19326	67.8	57	12.2	67.8	Ack19326 Human mic
25	9	ACI70251	67.8	58	12.2	67.8	Act70251 Human mic
27	3	AAA70510	67.8	59	12.2	67.8	Aaa70510 Novel hum
27	4	AAH78477	67.8	60	12.2	67.8	Aah78477 Nucleotid
27	8	ACC49274	67.8	61	12.2	67.8	Acc49274 Human RFR
29	3	AAZ35698	67.8	62	12.2	67.8	Aaz35698 Mouse imm
30	6	ABX68776	67.8	63	12.2	67.8	Abx68776 Novel Hel
30	14	ADN00258	67.8	64	12.2	67.8	Adn00258 PCR prime
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40	11	ADM96528	67.8	66	12.2	67.8	Adm96528 Oligonuc
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60	6	ABN59517	67.8	70	12.2	67.8	Abn59517 Human spl
60	6	ABN46001	67.8	71	12.2	67.8	Abn46001 Human spl
60	6	ABN44981	67.8	72	12.2	67.8	Abn44981 Human spl
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63	2	AAT00354	67.8	74	12.2	67.8	Aat00354 Family 3
65	6	ABN54413	67.8	75	12.2	67.8	Abn54413 Mouse spl
65	6	ABN29081	67.8	76	12.2	67.8	Abn29081 Rat splic
65	6	ABN53253	67.8	77	12.2	67.8	Abn53253 Mouse spl
22	2	AAT95476	66.7	78	12.2	66.7	Aat95476 Primer fo
22	12	ADL46145	66.7	79	12	66.7	Adl46145 HIV-1 gag
22	12	ADL46143	66.7	80	12	66.7	Adl46143 VSV G gly
25	9	ACH63932	66.7	81	12	66.7	Ach63932 DNA targ
30	2	AAT75519	66.7	82	12	66.7	Aat75519 3' primer
30	6	ABK27410	66.7	83	12	66.7	Abk27410 Human pap
30	6	ABK27409	66.7	84	12	66.7	Abk27409 Human pap
40	2	AAQ35140	66.7	85	12	66.7	Aaq35140 PCR prime
40	2	AAV09373	66.7	86	12	66.7	Aav09373 Rev and e
60	6	ABN36305	66.7	87	12	66.7	Abn36305 Human spl
60	6	ABN34729	66.7	88	12	66.7	Abn34729 Human spl
65	6	ABZ29819	65.6	89	12	65.6	Abz29819 Candida g
17	4	ABL47263	65.6	90	11.8	65.6	Ab147263 Human GRI
17	4	ABL47263	65.6	91	11.8	65.6	Ab147263 Human GRI
17	4	ABL47263	65.6	92	11.8	65.6	Ab147263 Human GRI

93 11.8 65.6 17 11 ADM54583  
C 94 11.8 65.6 17 14 AEB23697  
C 95 11.8 65.6 20 12 ADN58929  
96 11.8 65.6 20 12 ADN58929  
97 11.8 65.6 20 12 ADQ74729  
98 11.8 65.6 20 13 ADS19750  
C 99 11.8 65.6 20 13 ADS19683  
100 11.8 65.6 20 14 ADW44854

## ALIGNMENTS

RESULT 1  
AAH47976  
ID AAH47976 standard; DNA; 18 BP.  
XX  
AC AAH47976;  
XX  
XX 02-OCT-2001 (first entry)  
XX  
DE Human inducible NOS antisense oligonucleotide SEQ ID NO 20.  
XX  
DE Antisense oligonucleotide; inducible nitric oxide synthase; NOS;  
KW modulate expression; immunomodulator; antidiabetic; cardiovascular;  
KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
KW 2'-O-methoxyethyl; phosphorothioate; human; ss.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate backbone, 5' and 3' four  
FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine  
FT residues in the 2'-MOE wings are 5-methylcytidines) and a  
FT deoxy gap"  
XX  
XX W0200152902-Al.  
XX  
XX 26-JUL-2001.  
XX  
XX 15-JAN-2001; 2001WO-US001381.  
XX  
XX 24-JAN-2000; 2000US-00490208.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Bennett CF, Dean NM, Cowser LM;  
XX  
XX WPI; 2001-465340/50.  
XX  
XX New antisense oligonucleotides for modulating the expression of inducible  
PT nitric oxide synthase in cells or tissues, particularly useful for  
PT treating e.g. immunological, cardiovascular or neurological disorders, or  
PT ischaemia.  
XX  
XX Claim 3; Page 83; 144pp; English.  
XX  
XX The invention relates to antisense compounds, especially  
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible  
CC nitric oxide synthase and which specifically hybridise to and modulate  
CC expression of inducible nitric oxide synthase. The antisense compounds  
CC have immunomodulator, antidiabetic, cardiovascular, cardiant,  
CC neuroprotective, disorder and vasotropic activity. The antisense  
CC oligonucleotides are useful for inhibiting the expression of inducible  
CC nitric oxide synthase in cells or tissues. In particular, the antisense  
CC oligonucleotides are useful for treating diseases or disorders associated  
CC with inducible nitric oxide synthase, e.g. diabetes, immunological  
CC disorder, cardiovascular disorder, neurological disorder or  
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also  
CC useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a  
CC phosphorothioate backbone, a central "gap" region of ten nucleotides  
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine  
CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human  
CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)  
XX  
SQ Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCAG 18  
|||||  
Db 1 CTGCTAGAACTGCCAG 18

## RESULT 2

AD113013  
ID AD113013 standard; DNA; 22 BP.  
XX  
AC AD113013;  
XX  
XX 22-APR-2004 (first entry)  
XX  
DE PCR primer used to amplify human NOR-1 (MINOR) DNA SeqID 7.  
XX  
KW human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;  
KW atopic dermatitis; anti-allergic; anti-inflammatory; dermatological;  
KW primer.  
XX Homo sapiens.  
XX  
XX W02004003198-Al.  
XX  
XX 08-JAN-2004.  
XX  
XX 27-JUN-2003; 2003WO-JP008199.  
XX  
XX 27-JUN-2002; 2002JP-00188490.  
XX  
XX (GENO-) GENOX RES INC.  
XX (NIGE-) JAPAN GEN AGENCY NATION.  
XX  
XX Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;  
XX  
XX WPI; 2004-083057/08.  
XX  
XX Examining allergic diseases e.g. atopic dermatitis by differential  
PT display based on gene expression of NOR-1 receptor protein, also  
PT applicable in screening compounds for treatment of allergic diseases.  
XX  
XX Example 1; SEQ ID NO 7; 155pp; Japanese.  
XX  
XX This invention relates to a novel method for examining allergic diseases  
CC that comprises comparing the expression levels of a gene encoding the NOR  
CC -1 receptor protein between patients and healthy individuals.  
CC Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in  
CC the specialist white blood cells known as eosinophils and is involved in  
CC mediating an allergic reaction. The present invention describes a  
CC differential display method that can identify the expression level of  
CC this gene in order to identify its usefulness in diagnosing allergic  
CC diseases such as atopic dermatitis. Furthermore, compositions can also be  
CC used to screen compounds for the treatment of allergic diseases.  
CC Accordingly, they exhibit various activities including anti-allergic,  
CC anti-inflammatory and dermatological. This oligonucleotide sequence is a  
CC PCR primer used to amplify human NOR-1 DNA in an exemplification of the  
CC invention.  
XX  
SQ Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 22;  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTAGAACTGCCAG 18  
|||||  
Db 6 TGCTAGAACTGCAC 22

## RESULT 3

ABSS1490  
ID ABS1490 standard; cDNA; 76 BP.

XX AC

XX AC

XX DT

XX 21-OCT-2002 (first entry)

XX DE

XX Human cDNA encoding prey protein for Shigella ospC1 #15.

XX ss; gene; prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1;  
KW Shigella; shigellosis; bacillary dysentery; antibacterial;

KW yeast two-hybrid system; protein-protein interaction; SID;

KW selected interacting domain; human.

XX OS

XX Homo sapiens.

XX PN

XX WO200257303-A2.

XX PD

XX 25-JUL-2002.

XX PF

XX 11-JAN-2002; 2002WO-EP000777.

XX PR

XX 12-JAN-2001; 2001US-0261130P.

XX PA

XX (HYBR-) HYBRIGENICS.

XX PI

XX Legrain P;

XX DR

XX WPI; 2002-599706/64.

XX P-PSDB; ABG70097.

XX New complex of protein-protein interactions between a bait Shigella  
PT flexneri polypeptide and a prey mammalian or human placenta polypeptide  
PT for treating or preventing bacillary dysentery in a mammal or human.

PS Claim 8; Page 79; 162pp; English.

XX The invention relates to a complex of protein-protein interactions  
CC between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC,  
CC ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the  
CC specification. The complexes are formed using the yeast two-hybrid  
CC system. Also included are (1) a recombinant host cell expressing the  
CC interactions between the Shigella flexneri polypeptide and a mammalian  
CC polypeptide defined in the specification; (2) selecting a modulating  
CC compound that inhibits or activates the protein-protein interactions; (3)  
CC a modulating compound obtained from the method of (2); (4) a SID  
CC (selected interacting domain) polypeptide or its fragment or variant  
CC comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a  
CC SID polynucleotide or its fragment or variant comprising encoding the  
CC above polypeptides a vector comprising (5); (6) a recombinant host cell  
CC containing the vector; and (10) a protein chip comprising Shigella  
CC flexneri polypeptide and a mammalian polypeptide defined in the  
CC specification. A pharmaceutical composition comprising the compound,  
CC polypeptide or polynucleotide is useful for treating or preventing  
CC shigellosis (bacillary dysentery) in a human or mammal. The present  
CC sequence encodes a human prey protein isolated by the yeast two-hybrid  
CC assay, forming a complex of the invention with a shigella protein

XX SQ Sequence 76 BP; 18 A; 19 C; 20 G; 19 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 76;  
Best Local Similarity 88.9%; Pred. No. 5.9e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18

Db 20 CTTCTAGAAATGCCCG 37

## RESULT 4

ABNS4635

ID ABNS4635 standard; DNA; 65 BP.

XX AC

XX ABNS4635;

XX DT

XX 15-JUL-2002 (first entry)

XX DE

XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27383.

XX KW

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

XX splice variant; transcriptome; oligonucleotide library; ss.

XX OS

XX Mus musculus.

XX PN

XX WO200210449-A2.

XX PD

XX 07-FEB-2002.

XX PF

XX 20-JUL-2001; 2001WO-IB001903.

XX PR

XX 28-JUL-2000; 2000US-0221607P.

XX PA

XX 02-MAY-2001; 2001US-0287724P.

XX PI

XX (COMP-) COMPUGEN INC.

XX SH

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX PT

XX New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.

XX PS

XX Example 1; SEQ ID NO 27383; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABNS5989 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ

Sequence 65 BP; 9 A; 16 C; 17 G; 23 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 6; Length 65;  
Best Local Similarity 88.2%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCA 17





Best Local Similarity 93.3%; Pred. No. 3e+03; Mismatches 0; Indels 1; Gaps 0;  
Matches 14; Conservative 0;

Qy 1 CTGTCTAGAACTGCC 15  
|||||  
Db 4 CTGTCTAGAACTGCC 18

## RESULT 7

AA043849  
ID AAD43849 standard; DNA; 30 BP.

XX  
AC AAD43849;  
XX

DT 14-NOV-2002 (first entry)  
XX

XX Human HAH1 DNA amplifying PCR primer #2.  
XX

XX Single stranded polynucleotide tag; cleavage agent; gene expression;  
KW human; PCR; primer; ss.  
KW

XX Homo sapiens.  
OS

XX WO200259357-A2.  
PN

XX 01-AUG-2002.  
PD

XX 24-JAN-2002; 2002WO-DK000052.  
PF

XX 24-JAN-2001; 2001DK-00000126.  
PR

XX 12-FEB-2001; 2001US-0267704P.  
PR

XX (GENO-) GENOMIC EXPRESSION APS.  
PA

XX Pedersen ML;  
PI

XX WPI; 2002-636542/68.  
DR

XX Obtaining single stranded polynucleotide tags from a biological sample,  
PT for analyzing gene expression or diagnosing clinical conditions,  
PT comprises employing nicking endonucleases that cleave complementary  
PT strands.  
PT

XX Example; Page 293; 302pp; English.  
PS

XX The invention relates to a method for obtaining a single stranded  
CC polynucleotide tag from a biological sample by cleaving one of the  
CC complementary strands of a double stranded polynucleotide with a cleavage  
CC agent capable of recognising a double stranded polynucleotide comprising  
CC complementary strands and cleaving only one of the strands of the  
CC polynucleotide in the process of generating a single stranded  
CC polynucleotide tag. The method is useful for separating, analysing,  
CC quantifying or obtaining single stranded polynucleotides comprising tags  
CC originating partly, and preferably wholly from a source of DNA and/or RNA  
CC in a sample comprising biological cells. The method is particularly for  
CC analysing gene expression (expression profiling or differential gene  
CC expression), or in diagnosing clinical conditions. The present sequence  
CC is human HAH1 DNA amplifying PCR primer. This sequence is used in the  
CC exemplification of the invention  
XX

SQ Sequence 30 BP; 6 A; 10 C; 7 G; 7 T; 0 U; 0 Other;  
Query Match 74.4%; Score 13.4; DB 6; Length 30;

Best Local Similarity 93.3%; Pred. No. 3.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCGAG 18  
|||||  
Db 3 TCTAGAACTGCCGAG-17

## RESULT 8

ABN44109/c

ID ABN44109 standard; DNA; 60 BP.

XX  
AC ABN44109;  
XX

DT 15-JUL-2002 (first entry)  
XX

DE Human spliced transcript detection oligonucleotide SEQ ID NO:16857.  
XX

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
KW

XX Homo sapiens.  
OS

XX WO200210449-A2.  
PN

XX 07-FEB-2002.  
PD

XX 20-JUL-2001; 2001WO-IB001903.  
PF

XX 28-JUL-2000; 2000US-0221607P.  
PR

XX 02-MAY-2001; 2001US-0287724P.  
PR

XX (COMP-) COMPUGEN INC.  
PA

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WPI; 2002-257383/30.  
DR

XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
PT

XX Example 1; SEQ ID NO 16857; 47pp; English.  
PS

XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 60 BP; 20 A; 15 C; 14 G; 11 T; 0 U; 0 Other;  
Query Match 74.4%; Score 13.4; DB 6; Length 60;

Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCGAG 18  
|||||  
Db 16 TCTAGAACTGCCGAG 2

## RESULT 9

ADN58822

ID ADN58822 standard; DNA; 20 BP.

```

XX AC ADN58822;
XX DT 12-AUG-2004 (first entry)
XX DE Human B7H antisense oligonucleotide ISIS 205933.
XX KW B7H; autoimmune disease; ss; antisense; human.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2004102398-A1.
XX PD 27-MAY-2004.
XX PF 23-NOV-2002; 2002US-00303420.
XX PR 23-NOV-2002; 2002US-00303420.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Dobie KW;
XX DR WPI; 2004-399728/37.
XX PT New compound targeted to a nucleic acid molecule encoding B7H and
XX PT inhibits expression of B7H, useful for modulating the expression of B7H
XX PT or for diagnosing or treating, e.g. autoimmune disease.
XX PS Example 15; SEQ ID NO 73; 97pp; English.
XX CC The invention relates to a compound targeted to a nucleic acid molecule
XX CC encoding B7H, where the compound specifically hybridises with the nucleic
XX CC acid molecule encoding B7H and inhibits the expression of B7H. The
XX CC compound is useful for modulating the expression of B7H. It is also
XX CC useful for diagnosing or treating diseases associated with expression of
XX CC B7H, e.g. an autoimmune disease. The present sequence represents a human
XX CC B7H antisense oligonucleotide.
XX SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 12; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCCCG 18
   |||||
Db 1 CAGTCCAGGACTGCCCG 18

RESULT 10
AAx88302
ID AAX88302 standard; DNA; 24 BP.
AC AAX88302;
XX 28-SEP-1999 (first entry)
XX Human CD30 antigen binding domain PCR primer 1.
XX CD30; antigen binding domain; human; suppressor; cell proliferation;
XX tumour formation; metastasis; CD30-antigen expressing cell; antisense;
XX cellular activation; cell death; cell lysis; anticancer; treatment;
XX CD30-expressing tumour; amplification; PCR primer; ss.
XX Synthetic.
XX OS Homo sapiens.
XX DE19838967-A1.
XX 12-AUG-1999.
XX

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```

PF 06-FEB-1998; 98DE-01038967.
XX 06-FEB-1998; 98DE-01038967.
XX PA (ABKE/) ABKEN H.
XX PI Abken H;
XX DR WPI; 1999-445521/38.
XX Suppressing proliferation, tumor formation and metastasis of CD30-
XX positive cells by contact with specific binding agent, for treating
XX tumors.
XX Example 3; Page 3; 8pp; German.
XX This invention describes a novel method for the suppression of unlimited
XX proliferation, tumour formation and metastasis of CD30-antigen expressing
XX cells and uses a molecule (I) that binds specifically to CD30 without
XX causing cellular activation through CD30. (I) inhibit cell proliferation
XX by an antisense mechanism or, where (I) is an antibody, by induction of
XX cell death/lysis. CD30+ L540 lymphoma cells (104 ml-1) were incubated
XX with 10 mu g/ml of single-chain Fv anti-CD30 polypeptide, and after 6
XX days metabolism of tetrazolium salt to formazan measured to estimate cell
XX viability. (I) have anticancer activity and are used to treat CD30-
XX expressing tumours. This sequence represents a PCR primer used to amplify
XX the human CD30 antigen binding domain
XX SQ Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCCCG 18
   |||||
Db 7 CAGTCTAGAACTGCCCG 24

RESULT 11
ACI78021
ID ACI78021 standard; DNA; 25 BP.
AC ACI78021;
XX 14-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 78012.
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX OS Homo sapiens.
XX US2003104410-A1.
XX 05-JUN-2003.
XX 15-MAR-2002; 2002US-00098263.
XX 16-MAR-2001; 2001US-0276759P.
XX (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX

```

PS Claim 1; SEQ ID NO 78012; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX

SQ Sequence 25 BP; 6 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 25;  
Best Local Similarity 83.3%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCACG 18  
||| ||||| ||| |||

Db 8 CTCTCTAGAACTGCCAAG 25

RESULT 12

ABS52868

ID ABS52868 standard; DNA; 37 BP.

AC ABS52868;

XX

XX 27-NOV-2002 (first entry)

DE Plasmid pML-Ptac PCR primer #5.

XX

XX Expression control sequence; microbiology; operon leader; PCR; primer;  
bacterial gene expression; p-independent transcription terminator;  
pML-Ptac; ss.

OS Synthetic.

XX

XX EP1234893-A1.

PN

XX

PD 28-AUG-2002.

XX

XX 30-JAN-2002; 2002EP-00002298.

PF

XX

XX 22-FEB-2001; 2001RU-00104817.

PR

XX

PA (AJIN ) AJINOMOTO CO INC.

XX

XX Mashko SV, Zimenkov DV;

PI

XX

XX WPI; 2002-659523/71.

DR

XX

XX An expression control sequence which controls expression of a target gene linked downstream of the expression control sequence depending on an intracellular concentration of an amino.

PT

XX

PS Example 1; Page 11; 32pp; English.

XX

CC The invention relates to an expression control sequence which controls expression of a target gene linked downstream of the expression control sequence depending on an intracellular concentration of an amino acid. In the bacterium which harbours a DNA construct containing the expression control sequence, a promoter linked upstream and the target gene linked downstream of the expression control sequence, the frequency of termination of transcription is lowered by increase of an intracellular concentration of an amino acid whereby expression of the target gene increases. The expression sequence is useful for the microbiological industry in particular to the development of a new approach to the regulated gene expression in bacterial cells. The present sequence represents a PCR primer used to construct the plasmid pML-Ptac

XX

SQ Sequence 37 BP; 11 A; 11 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 37;  
Best Local Similarity 83.3%; Pred. No. 4.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCACG 18  
||| ||||| ||| |||

Db 4 CTGCTCTAGAACTGCCAAG 21

RESULT 13

ABZ04767

ID ABZ04767 standard; DNA; 50 BP.

XX

AC ABZ04767;

XX

XX 09-JAN-2003 (first entry)

DT

XX Human leukocyte gene expression profiling probe SEQ ID NO 4758.

DE

XX

XX T7; leukocyte; gene expression profiling; allograft rejection;  
atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
ss.

KW

XX

XX Homo sapiens.

OS

XX

XX WO200257414-A2.

PN

XX

XX 25-JUL-2002.

PD

XX

XX 22-OCT-2001; 2001WO-US047856.

PF

XX

XX 20-OCT-2000; 2000US-0241994P.

PR

XX

XX 08-JUN-2001; 2001US-0296764P.

PR

XX

PA (BIOC-) BIOCARDIA INC.

XX

XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
Ly N, Woodward R, Quettermous T, Johnson F;

PI

XX

XX WPI; 2002-636525/68.

DR

XX

XX New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

PT

XX

XX Claim 1; Page 480; Opp; English.

PS

XX

XX The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection,

CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
XX  
SQ Sequence 50 BP; 18 A; 17 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 50;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18  
Db 17 CAGACTACAAGTCCCG 34

## RESULT 14

ID ADP10075  
ADP10075 standard; DNA; 50 BP.  
XX  
AC ADP10075;  
XX  
DT 12-AUG-2004 (first entry)  
XX

DE 50-mer oligonucleotide marker probe of the invention #84.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;  
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.  
KW  
XX Homo sapiens.

OS  
XX WO2004042346-A2.

PN  
XX 21-MAY-2004.

XX 24-APR-2003; 2003WO-US012946.

XX 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;  
PI Rosenberg S;

XX WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,  
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant  
PT rejection, in an individual, comprises detecting the expression level of  
PT the genes.

XX Claim 2; SEQ ID NO 84; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant  
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual  
CC comprises detecting the expression level of one or more genes. The  
CC methods, system and kits are useful in diagnosing or monitoring  
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic  
CC islet, lung, bone marrow or stem cell transplant rejection,  
CC xenotransplant rejection or mechanical organ replacement rejection, in an  
CC individual. The method is also useful in assessing the immune status of  
CC an individual. The methods are also useful in diagnosing and monitoring  
CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
CC viral, bacterial or fungal infection. The present sequence represents a  
CC 50 mer oligonucleotide marker for diagnosis and monitoring of allograft  
CC rejection and other disorders.

XX Sequence 50 BP; 18 A; 17 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 12; Length 50;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18  
Db 17 CAGACTACAAGTCCCG 34

## RESULT 15

ABN35482  
ID ABN35482 standard; DNA; 60 BP.

XX  
AC ABN35482;

XX  
DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:8230.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

PN  
XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.

XX Example 1; SEQ ID NO 8230; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting  
PS messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
PS )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridizing selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 60 BP; 12 A; 15 C; 18 G; 15 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 60;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18

Db 9 CTGTCCAGCACTGCCTAG 26

RESULT 16  
ABN40069/c  
ID ABN40069 standard; DNA; 60 BP.

AC ABN40069;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:12817.

KW Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of a

PT genome, useful for detecting tissue-, pathology-, and developmental-

PT specific genes.

PS Example 1; SEQ ID NO 12817; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN2753 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 60 BP; 20 A; 13 C; 12 G; 15 T; 0 U; 0 Other;

XX Query Match 73.3%; Score 13.2; DB 6; Length 60;

XX Best Local Similarity 83.3%; Pred. No. 4.3e+03;

XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCAG 18

||||| ||||| ||||| |||||

Db 34 CTGTCTTGAAGTGTTCAG 17

RESULT 17

AAS00425/c

ID AAS00425 standard; DNA; 62 BP.

XX AAS00425;

XX AAS00425;

DT 11-MAY-2001 (first entry)

DE Human B7-3 5'-RT PCR primer.

XX Human; B7-3; inducible co-stimulator; ICOS; TU-D; KIAA0653; CD28; T-cell;

XX ICOS-mediated activity; IL-10 production; TH2 activity;

XX Helicobacter pylori induced peptic ulcer; Crohn's disease;

XX multiple sclerosis; type I diabetes mellitus; graft rejection;

XX helminth infection; allergic disease; PCR primer; ss.

XX Homo sapiens.

XX WO200112658-A2.

XX 22-FEB-2001.

XX 10-AUG-2000; 2000WO-GB003079.

XX 11-AUG-1999; 99US-0148402P.

XX (ISIS-) ISIS INNOVATIONS LTD.

XX Davis S;

XX WPI; 2001-226547/23.

XX New B7-3 polypeptides useful for modulating inducible co-stimulator

XX protein and for treating ulcers, Crohn's disease, multiple sclerosis,

XX diabetes mellitus, infections and allergic diseases.

XX Disclosure; Page 62; 77pp; English.

CC The present sequence for B7-3 5'-RT PCR primer is used with B7-3 3'-RT  
CC PCR primer (AAS00426) to amplify human B-cell RNA to isolate a novel B7-3  
CC protein which acts as a ligand for inducible co-stimulator (ICOS)  
CC protein. The B7-3 protein previously referred to as TU-D or KIAA0653 was  
CC considered by the 2 groups as being incomplete. The present inventor has  
CC determined the sequence to be complete and renamed the sequence as B7-3.  
CC Also described is a soluble form of B7-3 (AAU00423) which comprises the  
CC B7-3 signal sequence and extracellular domain. The extracellular domain  
CC is shown to bind ICOS which is related to CD28 and expressed on T-cells.  
CC B7-3 polypeptides or its fragments are useful for identifying a substance  
CC which interacts with the polypeptide or its fragment. B7-3 polypeptides,  
CC fragments, tetramer, an agent with an ability to affect B7-3 activity or  
CC a specific binding member are useful for modulating an ICOS-mediated  
CC activity of T-cells by modulating IL-10 production and TH2 activity, and  
CC for manufacturing a medicament for modulating an ICOS-mediated activity  
CC of T-cells. B7-3 polypeptides are useful for development of diagnostic,  
CC prophylactic and therapeutic agents for diseases such as Helicobacter  
CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type I  
CC diabetes mellitus, graft rejection, helminth infections, and allergic  
CC diseases

XX Sequence 62 BP; 13 A; 20 C; 17 G; 12 T; 0 U; 0 Other;

XX Query Match 73.3%; Score 13.2; DB 4; Length 62;

XX Best Local Similarity 83.3%; Pred. No. 4.3e+03;

XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCAG 18

||||| ||||| ||||| |||||

Db 62 CAGTCCAGCACTGCCAG 45

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RESULT 18
ABN56084
ID ABN56084 standard; DNA; 65 BP.
XX
AC ABN56084;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28832.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 28832; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 15 A; 16 C; 16 G; 18 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
| | | | | | | | | | | | | | | |
Db 2 CTGTCAGAAATGCTCAG 19
| | | | | | | | | | | | | | | |

RESULT 19
ABN54268/c
ID ABN54268 standard; DNA; 65 BP.
XX
AC ABN54268;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:27016.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 27016; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 13 A; 19 C; 13 G; 20 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
| | | | | | | | | | | | | | | |
Db 32 CTGTCAGAAATGACCAG 15
| | | | | | | | | | | | | | | |

RESULT 20
ACD93864

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RESULT 22  
AAF57115/C





PT New nucleic acid molecule that down-regulates expression of Grb2-related  
PT with insert domain (GRID) gene, useful for treating a condition  
PT associated with the level of GRID, e.g. tissue/graft rejection and  
PT leukemia.

XX Claim 4; SEQ ID NO 655; 74pp; English.

XX The invention relates to a nucleic acid molecule that down-regulates  
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a  
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNasezyme,  
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell  
CC including the novel nucleic acid molecule, reducing GRID activity in a  
CC cell by contacting the cell with the novel nucleic acid molecule,  
CC treating a patient having a condition associated with the level of GRID  
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with  
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by  
CC contacting the cell with the novel nucleic acid molecule, an expression  
CC vector comprising a nucleic acid sequences (encoding at least the novel  
CC nucleic acid molecule in a manner that allows its expression), a  
CC mammalian cell including the expression vector and an enzymatic nucleic  
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid  
CC molecule is useful for treating a condition associated with the level of  
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is  
CC a target region for the enzymatic nucleic acids of the invention.

XX SQ Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 11; Length 17;

Best Local Similarity 62.5%; Pred. No. 6.2e+03;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTCTAGAACTGCCCA 17

Db 1 UGUCUGGAGCGGCCA 16

RESULT 25

AEB23669/c

ID AEB23669 standard; DNA; 17 BP.

AC AEB23669;

DT 22-SEP-2005 (first entry)

DE HLA-DP allele identification-related oligonucleotide probe SeqID212.

KW HLA-DP; human leukocyte antigen; diagnostic; SNP detection;

KW DNA detection; transplant rejection; cancer; diabetes; probe; ss.

OS Homo sapiens.

PN JP2005185175-A.

PD 14-JUL-2005.

PF 25-DEC-2003; 2003JP-00430557.

PR 25-DEC-2003; 2003JP-00430557.

PA (CANO ) CANON KK.

PI Tsukada M;

DR WPI; 2005-515774/53.

XX Probe set for identifying human leukocyte antigen (HLA)-DP allele in test  
PT substance in patients with organ transplant, cancer, diabetes, comprises  
PT probes such as DPA1.010301, DPA1.010302, DPA1.0104, DPA1.0105,  
PT DPB1.010101, or DPB1.010102.

PS Claim 2; SEQ ID NO 212; 32pp; Japanese.

XX This invention relates to a novel probe set for identifying HLA-DP (human

CC leukocyte antigen-DP) alleles in a test substance. The invention enables  
CC identification of HLA-DP alleles in patients with organ transplant,  
CC cancer, diabetes and other multiple-factor diseases, and thus provides  
CC tailored medical treatment to individual patients. The present sequence  
CC is that of an oligonucleotide probe which is used in the HLA-DP probe set  
CC of the present invention.

XX SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 14; Length 17;

Best Local Similarity 87.5%; Pred. No. 6.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 16

Db 17 CTGTCCGGAAGTCCC 2

Search completed: March 3, 2006, 08:00:27

Job time : 124.534 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds  
(without alignments)  
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Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 cgtctagaactgccag 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	13.4	74.4	25	3	US-09-396-196G-5801
C 2	13.4	74.4	25	3	US-09-396-196G-5802
C 3	13.4	74.4	30	3	US-10-053-883-49
C 4	13.2	73.3	25	3	US-09-396-196G-29403
C 5	13.2	73.3	25	3	US-09-396-196G-29404
C 6	13.2	73.3	25	3	US-09-396-196G-113025
C 7	13.2	73.3	50	3	US-10-131-827-4758
C 8	13.2	73.3	53	6	PCT-US95-10219-13
C 9	13.2	73.3	53	6	PCT-US95-10219-13
C 10	13.2	73.3	60	2	US-08-282-030-15
C 11	13.2	73.3	60	6	PCT-US95-10219-15
C 12	12.8	71.1	20	3	US-09-060-299-76
C 13	12.8	71.1	20	3	US-09-402-923A-76
C 14	12.8	71.1	25	3	US-09-396-196G-24036
C 15	12.8	71.1	25	3	US-09-396-196G-86286
C 16	12.8	71.1	25	3	US-09-396-196G-108974
C 17	12.8	71.1	38	3	US-10-001-052-80
C 18	12.4	68.9	25	3	US-09-396-196G-5723
C 19	12.4	68.9	25	3	US-09-396-196G-5724
C 20	12.4	68.9	25	3	US-09-396-196G-12464
C 21	12.4	68.9	25	3	US-09-396-196G-12465
C 22	12.4	68.9	47	3	US-09-422-978-410
C 23	12.2	67.8	25	3	US-09-098-628-64
C 24	12.2	67.8	25	3	US-09-396-196G-5483

C 25	12.2	67.8	25	3	US-09-396-196G-5484	Sequence 5484, Ap
C 26	12.2	67.8	25	3	US-09-396-196G-41203	Sequence 41203, A
C 27	12.2	67.8	25	3	US-09-396-196G-52243	Sequence 52243, A
C 28	12.2	67.8	25	3	US-09-396-196G-97883	Sequence 97883, A
C 29	12.2	67.8	25	3	US-09-396-196G-97884	Sequence 97884, A
C 30	12.2	67.8	25	3	US-09-396-196G-124884	Sequence 124884, A
C 31	12.2	67.8	25	3	US-09-673-245-1	Sequence 1, Appl
C 32	12.2	67.8	50	3	US-10-131-827-6410	Sequence 6410, Ap
C 33	12.2	67.8	50	3	US-10-131-827-6800	Sequence 6800, Ap
C 34	12.2	67.8	62	3	US-08-687-421-402	Sequence 402, App
C 35	12	66.7	22	2	US-08-639-501-92	Sequence 92, Appl
C 36	12	66.7	22	2	US-09-044-948-92	Sequence 92, Appl
C 37	12	66.7	22	3	US-09-044-908-92	Sequence 92, Appl
C 38	12	66.7	30	2	US-08-458-120-4	Sequence 4, Appl
C 39	12	66.7	30	2	US-08-867-970-4	Sequence 4, Appl
C 40	12	66.7	30	3	US-09-326-217-4	Sequence 4, Appl
C 41	12	66.7	30	3	US-09-732-020-4	Sequence 4, Appl
C 42	12	66.7	30	3	US-09-876-256-10	Sequence 10, Appl
C 43	12	66.7	30	3	US-09-876-256-11	Sequence 11, Appl
C 44	12	66.7	40	2	US-08-147-890-10	Sequence 10, Appl
C 45	11.8	65.6	16	3	US-09-371-772B-6968	Sequence 6968, Ap
C 46	11.8	65.6	17	3	US-08-584-040-3750	Sequence 3750, Ap
C 47	11.8	65.6	17	3	US-09-371-772B-1517	Sequence 1517, Ap
C 48	11.8	65.6	17	3	US-09-371-772B-6132	Sequence 6132, Ap
C 49	11.8	65.6	17	3	US-09-685-664B-1517	Sequence 1517, Ap
C 50	11.8	65.6	25	3	US-09-396-196G-9380	Sequence 9380, Ap
C 51	11.8	65.6	25	3	US-09-396-196G-19933	Sequence 19933, A
C 52	11.8	65.6	25	3	US-09-396-196G-19934	Sequence 19934, A
C 53	11.8	65.6	25	3	US-09-396-196G-19935	Sequence 19935, A
C 54	11.8	65.6	25	3	US-09-396-196G-96302	Sequence 96302, A
C 55	11.8	65.6	25	3	US-09-396-196G-96303	Sequence 96303, A
C 56	11.8	65.6	25	3	US-09-396-196G-103286	Sequence 103286, A
C 57	11.8	65.6	25	3	US-09-396-196G-103287	Sequence 103287, A
C 58	11.8	65.6	25	3	US-09-396-196G-103288	Sequence 103288, A
C 59	11.8	65.6	25	3	US-09-396-196G-123769	Sequence 123769, A
C 60	11.8	65.6	27	3	US-09-023-045-8	Sequence 8, Appl
C 61	11.8	65.6	27	3	US-09-435-321-8	Sequence 8, Appl
C 62	11.8	65.6	28	3	US-09-940-244-237	Sequence 297, Ap
C 63	11.8	65.6	28	3	US-09-777-430C-35	Sequence 33, Appl
C 64	11.8	65.6	30	2	US-08-276-852-28	Sequence 28, Appl
C 65	11.8	65.6	30	2	US-08-133-011-35	Sequence 35, Appl
C 66	11.8	65.6	30	2	US-08-437-815-7	Sequence 7, Appl
C 67	11.8	65.6	30	2	US-08-322-730A-35	Sequence 35, Appl
C 68	11.8	65.6	30	2	US-08-162-102C-16	Sequence 16, Appl
C 69	11.8	65.6	30	2	US-08-387-874-35	Sequence 35, Appl
C 70	11.8	65.6	30	2	US-08-899-575-28	Sequence 28, Appl
C 71	11.8	65.6	30	2	US-08-899-575-28	Sequence 28, Appl
C 72	11.8	65.6	30	2	US-08-897-040-7	Sequence 7, Appl
C 73	11.8	65.6	30	2	US-08-383-619-35	Sequence 35, Appl
C 74	11.8	65.6	30	3	US-08-907-739-35	Sequence 35, Appl
C 75	11.8	65.6	30	3	US-08-972-564-14	Sequence 14, Appl
C 76	11.8	65.6	30	3	US-09-386-642-56	Sequence 56, Appl
C 77	11.8	65.6	30	3	US-09-728-597-35	Sequence 35, Appl
C 78	11.8	65.6	30	3	US-08-920-100B-16	Sequence 16, Appl
C 79	11.8	65.6	30	6	PCT-US93-08364-35	Sequence 35, Appl
C 80	11.8	65.6	30	6	PCT-US93-08786-16	Sequence 16, Appl
C 81	11.8	65.6	30	6	PCT-US95-00667-16	Sequence 16, Appl
C 82	11.8	65.6	30	6	PCT-US95-08743-28	Sequence 28, Appl
C 83	11.8	65.6	34	3	US-09-481-620A-99	Sequence 99, Appl
C 84	11.8	65.6	42	3	US-09-139-802-213	Sequence 213, App
C 85	11.8	65.6	42	3	US-09-139-802-214	Sequence 214, App
C 86	11.8	65.6	42	3	US-09-139-802-215	Sequence 215, App
C 87	11.8	65.6	42	3	US-09-659-786-213	Sequence 213, App
C 88	11.8	65.6	42	3	US-09-659-786-214	Sequence 214, App
C 89	11.8	65.6	42	3	US-09-659-786-215	Sequence 215, App
C 90	11.8	65.6	42	3	US-09-889-480A-15	Sequence 15, Appl
C 91	11.8	65.6	44	3	US-09-139-802-216	Sequence 216, App
C 92	11.8	65.6	44	3	US-09-659-786-216	Sequence 216, App
C 93	11.8	65.6	47	9	5217864-5	Patent No. 5217864
C 94	11.8	65.6	50	3	US-10-131-827-6174	Sequence 6174, Ap
C 95	11.8	65.6	51	3	US-08-676-818-24	Sequence 24, Appl
C 96	11.8	65.6	51	3	US-09-407-549-24	Sequence 24, Appl
C 97	11.8	65.6	51	3	US-09-407-728-24	Sequence 24, Appl

c 98 11.8 65.6 65 2 US-08-468-012A-4 Sequence 4, Appli  
c 99 11.8 65.6 65 3 US-09-054-989-4 Sequence 4, Appli  
c 100 11.8 65.6 65 3 US-09-662-746A-4 Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-09-396-196G-5801/c  
; Sequence 5801, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5801  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-5801

Query Match 74.4%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15  
Db 21 CTGTCTAGAGTGCC 7

RESULT 2  
US-09-396-196G-5802/c  
; Sequence 5802, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5802  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-5802

Query Match 74.4%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15  
Db 15 CTGTCTAGAGTGCC 1

RESULT 3

US-10-053-883-49  
; Sequence 49, Application US/10053883  
; Patent No. 6958217  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN=1A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 49  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-053-883-49

Query Match 74.4%; Score 13.4; DB 3; Length 30;  
Best Local Similarity 93.3%; Pred. No. 5.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCCACG 18  
Db 3 TCTAGAACTGCCAAG 17

RESULT 4  
US-09-396-196G-29403/c  
; Sequence 29403, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29403  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-29403

Query Match 73.3%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCACG 18  
Db 25 CTGTCTAGAACTGCCACG 8

RESULT 5  
US-09-396-196G-29404/c  
; Sequence 29404, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.

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; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29404

Query Match      73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 23 CTGTGTAATACTGCACG 6

RESULT 6
US-09-396-196G-113025/c
; Sequence 113025, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113025
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-113025

Query Match      73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 21 CTGTCCAGAAATGACCAG 4

RESULT 7
US-10-131-827-4758
; Sequence 4758, Application US/10111827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08

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; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4758
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4758

Query Match      73.3%; Score 13.2; DB 3; Length 50;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 17 CAGACTACAACCTGCCCG 34

RESULT 8
US-08-282-030-13
; Sequence 13, Application US/08282030
; Patent No. 5589364
; GENERAL INFORMATION:
; APPLICANT: Williams, Jon I.
; APPLICANT: Pierce, James C.
; APPLICANT: Anderson, Mark G.
; APPLICANT: Kari, Prasad
; TITLE OF INVENTION: Recombinant Production of Biologically
; TITLE OF INVENTION: Active Peptides and Proteins
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,030
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-282-030-13

Query Match      73.3%; Score 13.2; DB 2; Length 53;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 15 CTGTCTAAAACCTGCTAAG 32

RESULT 9
PCT-US95-10219-13
; Sequence 13, Application PC/TUS9510219

```

GENERAL INFORMATION:  
APPLICANT: Williams, Jon I.  
APPLICANT: Pierce, James C.  
APPLICANT: Anderson, Mark G.  
APPLICANT: Kari, Prasad  
TITLE OF INVENTION: Recombinant Production of Biologically  
TITLE OF INVENTION: Active Peptides and Proteins  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10219  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,030  
FILING DATE: 29-JUL-1994  
NAME: Fordis, Jean B.  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0001-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-10219-13

Query Match 73.3%; Score 13.2; DB 6; Length 53;  
Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18  
|||||  
Db 15 CTGCTAAACTGCTAAG 32

RESULT 10  
US-08-282-030-15/c  
Sequence 15, Application US/08282030  
Patent No. 5589364  
GENERAL INFORMATION:  
APPLICANT: Williams, Jon I.  
APPLICANT: Pierce, James C.  
APPLICANT: Anderson, Mark G.  
APPLICANT: Kari, Prasad  
TITLE OF INVENTION: Recombinant Production of Biologically  
TITLE OF INVENTION: Active Peptides and Proteins  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,030  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fordis, Jean B.  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0001-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 60 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-282-030-15

Query Match 73.3%; Score 13.2; DB 2; Length 60;  
Best Local Similarity 83.3%; Pred. No. 7.9e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18  
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Db 50 CTGCTAAACTGCTAAG 33

RESULT 11  
PCT-US95-10219-15/c  
Sequence 15, Application PC/TUS9510219  
GENERAL INFORMATION:  
APPLICANT: Williams, Jon I.  
APPLICANT: Pierce, James C.  
APPLICANT: Anderson, Mark G.  
APPLICANT: Kari, Prasad  
TITLE OF INVENTION: Recombinant Production of Biologically  
TITLE OF INVENTION: Active Peptides and Proteins  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10219  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/282,030  
FILING DATE: 29-JUL-1994  
NAME: Fordis, Jean B.  
REGISTRATION NUMBER: 32,984  
REFERENCE/DOCKET NUMBER: 05387.0001-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 60 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-10219-15

Query Match 73.3%; Score 13.2; DB 6; Length 60;  
Best Local Similarity 83.3%; Pred. No. 7.9e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18  
||||| ||||| ||  
Db 50 CTGCTAAACTGCTAG 33

RESULT 12

US-09-060-299-76  
Sequence 76, Application US/09060299  
Patent No. 6545137  
GENERAL INFORMATION:

APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Merriman, Tony R  
APPLICANT: Metzker, Michael L  
TITLE OF INVENTION: No. 6545137el Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,299  
FILING DATE: 15-APR-1998  
CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-060-299-76  
Query Match 71.1%; Score 12.8; DB 3; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTAGAACTGCCAG 18  
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Db 4 GTCTGAACTTCCAG 19

RESULT 13

US-09-402-923A-76  
Sequence 76, Application US/09402923A  
Patent No. 655654  
GENERAL INFORMATION:

APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Merriman, Tony R  
APPLICANT: Metzker, Michael L  
TITLE OF INVENTION: No. 655654el LDL-Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 655654th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,923A  
FILING DATE: 14-Feb-2001

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01102  
FILING DATE: 15-APR-1998  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-81  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-402-923A-76  
Query Match 71.1%; Score 12.8; DB 3; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTAGAACTGCCAG 18  
||||| ||||| |||||  
Db 4 GTCTGAACTTCCAG 19

RESULT 14

US-09-396-196G-24036  
Sequence 24036, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittmann





Qy 5 CTAGAACTGCCAG 18  
||| |||||  
Db 8 CTAAGAACTGCCAG 21

## RESULT 19

US-09-396-196G-5724  
; Sequence 5724, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5724

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-5724

Query Match 68.9%; Score 12.4; DB 3; Length 25;

Best Local Similarity 92.9%; Pred. No. 2e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTAGAACTGCCAG 18

||| |||||

Db 2 CTAAGAACTGCCAG 15

## RESULT 20

US-09-396-196G-12464

; Sequence 12464, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12464

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-12464

Query Match 68.9%; Score 12.4; DB 3; Length 25;

Best Local Similarity 92.9%; Pred. No. 2e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCCA 17

||| |||||

Db 8 TCCAGAACTGCCCA 21

## RESULT 21

US-09-396-196G-12465

; Sequence 12465, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12465

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-12465

Query Match 68.9%; Score 12.4; DB 3; Length 25;

Best Local Similarity 92.9%; Pred. No. 2e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCCA 17

||| |||||

Db 2 TCCAGAACTGCCCA 15

## RESULT 22

US-09-422-978-410

; Sequence 410, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CP1

; CURRENT APPLICATION NUMBER: US/09/422,978

; PRIOR FILING DATE: 1999-10-20

; PRIOR FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 410

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 24

; OTHER INFORMATION: 99-1469-47 : polymorphic base G or C

US-09-422-978-410

Query Match 68.9%; Score 12.4; DB 3; Length 47;

Best Local Similarity 81.2%; Pred. No. 2.1e+03;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCC 16

||| |||||

Db 11 CTGCTAGAACTGSAC 26

## RESULT 23

US-09-098-628-64

; Sequence 64, Application US/09098628

; Patent No. 6294359

; GENERAL INFORMATION:

; APPLICANT: FIDDES, J.C.

; APPLICANT: ABRAHAM, J.D.  
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
; TITLE OF INVENTION: FACTOR ANALOG  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/098,628  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 21900-20089.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-098-628-64

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17  
||| ||| ||| ||| |||  
Db 9 CTGCTCGAACTGGCA 25

RESULT 24  
US-09-396-196G-5483/c  
; Sequence 5483, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5483  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-09-396-196G-5483

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 CTGCTAGAACTGCCCA 17  
||| ||| ||| ||| |||  
Db 24 CTTCTGGGACTGCCCA 8  
RESULT 25  
US-09-396-196G-5484/c  
; Sequence 5484, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5484  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-09-396-196G-5484

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
Best Local Similarity 82.4%; Pred. No. 2.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17  
||| ||| ||| ||| |||  
Db 23 CTTCTGGGACTGCCCA 7

Search completed: March 3, 2006, 07:34:53  
Job time : 24.6441 secs

GenCore version 5.1.7  
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QM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds  
(without alignments)  
673.188 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 cgtctgaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA.Main.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	9	US-10-182-049-20
2	15.4	85.6	22	8	US-10-608-863-7
3	15.4	85.6	25	8	US-10-719-900-409560
4	14.8	82.2	25	7	US-10-719-956-464843
5	14.8	82.2	25	7	US-10-719-956-596880
6	14.8	82.2	25	8	US-10-719-900-647319
7	14.8	82.2	25	5	US-10-043-487-70
8	14.4	80.0	25	7	US-10-719-956-44720
9	14.4	80.0	25	7	US-10-719-956-199852
10	14.4	80.0	25	7	US-10-719-956-425140
11	14.4	80.0	25	7	US-10-719-956-506614
12	14.4	80.0	25	7	US-10-719-956-563766
13	14	77.8	25	8	US-10-719-900-463026
14	14	77.8	25	8	US-10-719-900-492613
15	14	77.8	25	10	US-11-036-317-789153
16	13.8	76.7	25	7	US-10-719-956-30344
17	13.8	76.7	25	7	US-10-719-956-433626
18	13.8	76.7	25	7	US-10-719-956-566856
19	13.8	76.7	25	7	US-10-719-956-637106
20	13.8	76.7	25	7	US-10-719-956-683368
21	13.8	76.7	25	7	US-10-719-956-687023
22	13.8	76.7	25	8	US-10-719-900-3641
23	13.8	76.7	25	8	US-10-719-900-391493

Sequence 409559,	25	8	US-10-719-900-409559	76.7	13.8	24
Sequence 714062,	25	8	US-10-719-900-714062	76.7	13.8	25
Sequence 160516,	25	9	US-10-956-157-160516	76.7	13.8	26
Sequence 210346,	25	9	US-10-956-157-210346	76.7	13.8	27
Sequence 256211,	25	9	US-10-956-157-256211	76.7	13.8	28
Sequence 231756,	25	9	US-10-956-157-231756	76.7	13.8	29
Sequence 821377,	25	10	US-11-036-317-821377	76.7	13.8	30
Sequence 188296,	25	10	US-11-060-756-188296	76.7	13.8	31
Sequence 27383, A	65	3	US-09-908-975-27383	76.7	13.8	32
Sequence 211, App	20	7	US-10-280-183A-211	74.4	13.4	33
Sequence 205839,	25	7	US-10-719-956-205839	74.4	13.4	34
Sequence 454386,	25	7	US-10-719-956-454386	74.4	13.4	35
Sequence 81189, A	25	8	US-10-719-900-81189	74.4	13.4	36
Sequence 131894,	25	8	US-10-719-900-131894	74.4	13.4	37
Sequence 192759,	25	8	US-10-719-900-192759	74.4	13.4	38
Sequence 613650,	25	8	US-10-719-900-613650	74.4	13.4	39
Sequence 722102,	25	8	US-10-719-900-722102	74.4	13.4	40
Sequence 819672,	25	8	US-10-719-900-819672	74.4	13.4	41
Sequence 5801, App	25	9	US-10-809-189-5801	74.4	13.4	42
Sequence 5802, Ap	25	9	US-10-809-189-5802	74.4	13.4	43
Sequence 164909,	25	9	US-10-956-157-164909	74.4	13.4	44
Sequence 49, Appl	30	5	US-10-053-883-49	74.4	13.4	45
Sequence 16857, A	60	3	US-09-908-975-16857	74.4	13.4	46
Sequence 73, Appl	20	7	US-10-303-420-73	73.3	13.2	47
Sequence 78012, A	20	7	US-10-098-263B-78012	73.3	13.2	48
Sequence 159349,	25	5	US-10-719-956-159349	73.3	13.2	49
Sequence 159350,	25	7	US-10-719-956-159350	73.3	13.2	50
Sequence 249505,	25	7	US-10-719-956-249505	73.3	13.2	51
Sequence 464842,	25	7	US-10-719-956-464842	73.3	13.2	52
Sequence 596881,	25	7	US-10-719-956-596881	73.3	13.2	53
Sequence 55893, A	25	8	US-10-719-900-55893	73.3	13.2	54
Sequence 268396,	25	8	US-10-719-900-268396	73.3	13.2	55
Sequence 305146,	25	8	US-10-719-900-305146	73.3	13.2	56
Sequence 305147,	25	8	US-10-719-900-305147	73.3	13.2	57
Sequence 427474,	25	8	US-10-719-900-427474	73.3	13.2	58
Sequence 447134,	25	8	US-10-719-900-447134	73.3	13.2	59
Sequence 474762,	25	8	US-10-719-900-474762	73.3	13.2	60
Sequence 647318,	25	8	US-10-719-900-647318	73.3	13.2	61
Sequence 730151,	25	8	US-10-719-900-730151	73.3	13.2	62
Sequence 831370,	25	8	US-10-719-900-831370	73.3	13.2	63
Sequence 831371,	25	8	US-10-719-900-831371	73.3	13.2	64
Sequence 834909,	25	8	US-10-719-900-834909	73.3	13.2	65
Sequence 29403, A	25	9	US-10-809-189-29403	73.3	13.2	66
Sequence 29404, A	25	9	US-10-809-189-29404	73.3	13.2	67
Sequence 113025,	25	9	US-10-809-189-113025	73.3	13.2	68
Sequence 197861,	25	9	US-10-956-157-197861	73.3	13.2	69
Sequence 198885,	25	9	US-10-956-157-198885	73.3	13.2	70
Sequence 217325,	25	9	US-10-956-157-217325	73.3	13.2	71
Sequence 38997, A	25	10	US-11-036-317-38997	73.3	13.2	72
Sequence 83526, A	25	10	US-11-036-317-83526	73.3	13.2	73
Sequence 412135,	25	10	US-11-036-317-412135	73.3	13.2	74
Sequence 446749,	25	10	US-11-036-317-446749	73.3	13.2	75
Sequence 587266,	25	10	US-11-036-317-587266	73.3	13.2	76
Sequence 618048,	25	10	US-11-036-317-618048	73.3	13.2	77
Sequence 695245,	25	10	US-11-036-317-695245	73.3	13.2	78
Sequence 108950,	25	10	US-11-036-317-108950	73.3	13.2	79
Sequence 116937,	25	10	US-11-060-756-116937	73.3	13.2	80
Sequence 158473,	25	10	US-11-060-756-158473	73.3	13.2	81
Sequence 202905,	25	10	US-11-060-756-202905	73.3	13.2	82
Sequence 258462,	25	10	US-11-060-756-258462	73.3	13.2	83
Sequence 263749,	25	10	US-11-060-756-263749	73.3	13.2	84
Sequence 273810,	25	10	US-11-060-756-273810	73.3	13.2	85
Sequence 12, Appl	37	5	US-10-068-851-12	73.3	13.2	86
Sequence 4758, Ap	50	6	US-10-131-827-4758	73.3	13.2	87
Sequence 8230, Ap	60	3	US-09-908-975-8230	73.3	13.2	88
Sequence 12817, A	60	3	US-09-908-975-12817	73.3	13.2	89
Sequence 27016, A	65	3	US-09-908-975-27016	73.3	13.2	90
Sequence 28832, A	65	3	US-09-908-975-28832	73.3	13.2	91
Sequence 265514,	25	7	US-10-719-956-265514	73.3	13.2	92
Sequence 329291,	25	7	US-10-719-956-329291	73.3	13.2	93
Sequence 915056,	25	7	US-10-719-900-915056	73.3	13.2	94
Sequence 655, App	17	3	US-09-792-818-655	71.1	12.8	95



; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 596880  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-596880

Query Match 82.2%; Score 14.8; DB 7; Length 25;  
 Best Local Similarity 88.9%; Pred. No. 4.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18  
 |||||  
 Db 24 CTGGCTAGACTGCCCG 7

RESULT 6  
 US-10-719-900-647319  
 ; Sequence 647319, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 647319  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-647319

Query Match 82.2%; Score 14.8; DB 8; Length 25;  
 Best Local Similarity 88.9%; Pred. No. 4.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18  
 |||||  
 Db 8 CTCTCTAGAACTGCCCG 25

RESULT 7  
 US-10-043-487-70  
 ; Sequence 70, Application US/10043487  
 ; Publication No. US20030055220A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HYBRIGENICS  
 ; APPLICANT: Pierre, LEGRAIN  
 ; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptides  
 ; FILE REFERENCE: B4778A  
 ; CURRENT APPLICATION NUMBER: US/10/043,487  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,130  
 ; PRIOR FILING DATE: 2001-01-12  
 ; NUMBER OF SEQ ID NOS: 561  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 70  
 ; LENGTH: 76  
 ; TYPE: DNA  
 ; ORGANISM: Shigella flexneri  
 US-10-043-487-70

Query Match 82.2%; Score 14.8; DB 5; Length 76;  
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CTGCTAGAACTGCCCG 18  
 |||||  
 Db 20 CTTTCTAGAAATGCCCG 37

RESULT 8  
 US-10-719-956-44720  
 ; Sequence 44720, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 44720  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-44720

Query Match 80.0%; Score 14.4; DB 7; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 7.9e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 16  
 |||||  
 Db 6 CTGCTAGAACTGCCCG 21

RESULT 9  
 US-10-719-956-199852/c  
 ; Sequence 199852, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,956  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,836  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 699466  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 199852  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-10-719-956-199852

Query Match 80.0%; Score 14.4; DB 7; Length 25;  
 Best Local Similarity 93.8%; Pred. No. 7.9e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 16  
 |||||  
 Db 22 CTGCTAGAACTGCCCG 7

RESULT 10  
 US-10-719-956-425140  
 ; Sequence 425140, Application US/10719956  
 ; Publication No. US20040146910A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
 ; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 425140  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-425140

Query Match 80.0%; Score 14.4; DB 7; Length 25;  
Best Local Similarity 93.8%; Pred. No. 7.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 16  
Db 9 CTGTCCAGAACTGCC 24

## RESULT 11

US-10-719-956-506614/c  
; Sequence 506614, Application US/10/19956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 506614  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-506614

Query Match 80.0%; Score 14.4; DB 7; Length 25;  
Best Local Similarity 93.8%; Pred. No. 7.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 16  
Db 16 CTGTCTAGAACTGCAC 1

## RESULT 12

US-10-719-956-563766  
; Sequence 563766, Application US/10/19956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 563766  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-563766

Query Match 80.0%; Score 14.4; DB 7; Length 25;  
Best Local Similarity 93.8%; Pred. No. 7.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTAGAACTGCCCA 17  
Db 4 TGCTAGAACTGCCCA 19  
; Sequence 463026, Application US/10/19900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 463026  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-463026

Query Match 77.8%; Score 14; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTAGAACTGCCCAG 18  
Db 16 CTAGAACTGCCCAG 3

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US-10-719-900-492613/c  
; Sequence 492613, Application US/10/19900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 492613  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-492613

Query Match 77.8%; Score 14; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCCCA 17  
Db 20 TCTAGAACTGCCCA 7

## RESULT 15

US-11-036-317-789153/c  
; Sequence 789153, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1

Query Match 80.0%; Score 14.4; DB 7; Length 25;  
Best Local Similarity 93.8%; Pred. No. 7.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICANT: ADE MEI ZHOU  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956





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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 714062
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-714062

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Query Match      76.7%  Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%  Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 TGTCTAGAACTGCCCG 18
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Db      23 TGTGTAGAACTGTCCAG 7

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Job time : 222.11 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds  
(without alignments)  
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Title: US-10-655-801-20

Perfect score: 18  
Sequence: 1 ctgtctagaactgcccag 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	14.8	82.2	25	12	US-11-121-849-107523
2	14.8	82.2	25	12	US-11-136-527-339204
3	13.8	76.7	22	8	US-10-310-914A-925402
4	13.8	76.7	25	12	US-11-121-849-9721
5	13.8	76.7	25	12	US-11-121-849-297925
6	13.8	76.7	25	12	US-11-121-849-366615
7	13.8	76.7	25	12	US-11-136-527-127254
8	13.8	76.7	25	12	US-11-136-527-321780
9	13.8	76.7	25	12	US-11-136-527-330649
10	13.8	76.7	50	12	US-11-175-859-98954
11	13.4	74.4	19	8	US-10-310-914A-1209005
12	13.4	74.4	19	10	US-11-101-244-47652
13	13.4	74.4	19	10	US-11-101-244-365369
14	13.4	74.4	19	10	US-11-101-244-978416
15	13.4	74.4	19	11	US-11-083-784-47652
16	13.4	74.4	19	11	US-11-083-784-365369
17	13.4	74.4	19	11	US-11-083-784-978416
18	13.4	74.4	21	8	US-10-310-914A-535346
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20	13.4	74.4	25	12	US-11-121-849-76084

25	12	US-11-121-849-76085	74.4	c 21	Sequence 76085, A
25	12	US-11-121-849-360704	74.4	c 22	Sequence 360704, A
25	12	US-11-136-527-116504	74.4	c 23	Sequence 116504, A
25	12	US-11-136-527-116505	74.4	c 24	Sequence 116505, A
25	12	US-11-136-527-235336	74.4	c 25	Sequence 235336, A
30	12	US-11-193-528-49	74.4	c 26	Sequence 49, Appl
50	12	US-11-175-859-3381	74.4	c 27	Sequence 3381, A
50	12	US-11-175-859-15438	74.4	c 28	Sequence 15438, A
22	8	US-10-310-914A-456967	73.3	c 29	Sequence 456967, A
22	8	US-10-310-914A-611488	73.3	c 30	Sequence 611488, A
22	8	US-10-310-914A-762370	73.3	c 31	Sequence 762370, A
24	8	US-10-310-914A-357535	73.3	c 32	Sequence 357535, A
25	12	US-11-121-849-170920	73.3	c 33	Sequence 170920, A
25	12	US-11-121-849-193150	73.3	c 34	Sequence 193150, A
25	12	US-11-121-849-193194	73.3	c 35	Sequence 193194, A
25	12	US-11-121-849-276262	73.3	c 36	Sequence 276262, A
25	12	US-11-121-849-357010	73.3	c 37	Sequence 357010, A
25	12	US-11-121-849-517451	73.3	c 38	Sequence 517451, A
25	12	US-11-121-849-672213	73.3	c 39	Sequence 672213, A
25	12	US-11-121-849-672541	73.3	c 40	Sequence 672541, A
25	12	US-11-121-849-672542	73.3	c 41	Sequence 672542, A
25	12	US-11-136-527-339707	73.3	c 42	Sequence 339707, A
25	12	US-11-136-527-339726	73.3	c 43	Sequence 339726, A
37	12	US-11-002-141-12	73.3	c 44	Sequence 12, Appl
68	8	US-10-310-914A-13907	73.3	c 45	Sequence 13907, A
79	8	US-10-310-914A-9432	73.3	c 46	Sequence 9432, Ap
79	8	US-10-310-914A-4844	73.3	c 47	Sequence 4844, Ap
23	8	US-10-310-914A-535341	72.2	c 48	Sequence 535341, A
18	8	US-10-310-914A-439332	71.1	c 49	Sequence 439332, A
19	10	US-10-310-914A-1307598	71.1	c 50	Sequence 1307598, A
19	10	US-11-101-244-156956	71.1	c 51	Sequence 156956, A
19	10	US-11-101-244-289621	71.1	c 52	Sequence 289621, A
19	10	US-11-101-244-466854	71.1	c 53	Sequence 466854, A
19	10	US-11-101-244-783242	71.1	c 54	Sequence 783242, A
19	10	US-11-101-244-865598	71.1	c 55	Sequence 865598, A
19	10	US-11-101-244-865610	71.1	c 56	Sequence 865610, A
19	11	US-11-083-784-156956	71.1	c 57	Sequence 156956, A
19	11	US-11-083-784-289621	71.1	c 58	Sequence 289621, A
19	11	US-11-083-784-466854	71.1	c 59	Sequence 466854, A
19	11	US-11-083-784-783242	71.1	c 60	Sequence 783242, A
19	11	US-11-083-784-865598	71.1	c 61	Sequence 865598, A
19	11	US-11-083-784-865610	71.1	c 62	Sequence 865610, A
20	8	US-10-310-914A-418107	71.1	c 63	Sequence 418107, A
21	8	US-10-310-914A-461469	71.1	c 64	Sequence 461469, A
22	8	US-10-310-914A-667101	71.1	c 65	Sequence 667101, A
22	8	US-10-310-914A-925422	71.1	c 66	Sequence 925422, A
23	8	US-10-310-914A-362001	71.1	c 67	Sequence 362001, A
24	8	US-10-310-914A-667116	71.1	c 68	Sequence 667116, A
24	8	US-10-310-914A-979076	71.1	c 69	Sequence 979076, A
25	12	US-11-121-849-39028	71.1	c 70	Sequence 39028, A
25	12	US-11-121-849-43680	71.1	c 71	Sequence 43680, A
25	12	US-11-121-849-111621	71.1	c 72	Sequence 111621, A
25	12	US-11-121-849-170075	71.1	c 73	Sequence 170075, A
25	12	US-11-121-849-366614	71.1	c 74	Sequence 366614, A
25	12	US-11-121-849-419603	71.1	c 75	Sequence 419603, A
25	12	US-11-136-527-61681	71.1	c 76	Sequence 61681, A
25	12	US-11-136-527-358001	71.1	c 77	Sequence 358001, A
25	12	US-11-136-527-258022	71.1	c 78	Sequence 258022, A
25	12	US-11-136-527-336361	71.1	c 79	Sequence 336361, A
50	12	US-11-175-859-34375	71.1	c 80	Sequence 34375, A
19	8	US-11-175-859-40946	68.9	c 81	Sequence 40946, A
19	10	US-10-310-914A-671437	68.9	c 82	Sequence 671437, A
19	10	US-11-101-244-184742	68.9	c 83	Sequence 184742, A
19	10	US-11-101-244-352238	68.9	c 84	Sequence 352238, A
19	10	US-11-101-244-525775	68.9	c 85	Sequence 525775, A
19	10	US-11-101-244-865634	68.9	c 86	Sequence 865634, A
19	10	US-11-101-244-867750	68.9	c 87	Sequence 867750, A
19	10	US-11-101-244-867777	68.9	c 88	Sequence 867777, A
19	10	US-11-101-244-147150	68.9	c 89	Sequence 147150, A
19	11	US-11-083-784-184742	68.9	c 90	Sequence 184742, A
19	11	US-11-083-784-352238	68.9	c 91	Sequence 352238, A
19	11	US-11-083-784-525775	68.9	c 92	Sequence 525775, A
19	11	US-11-083-784-525775	68.9	c 93	Sequence 525775, A

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c 95 12.4 68.9 19 11 US-11-083-784-867750 Sequence 867750,  
c 96 12.4 68.9 19 11 US-11-083-784-867777 Sequence 867777,  
c 97 12.4 68.9 19 11 US-11-083-784-1417150 Sequence 1417150,  
c 98 12.4 68.9 20 8 US-10-310-914A-782986 Sequence 782986,  
c 99 12.4 68.9 21 8 US-10-310-914A-361952 Sequence 361952,  
c 100 12.4 68.9 23 8 US-10-310-914A-782849 Sequence 782849,

## ALIGNMENTS

## RESULT 1

US-11-121-849-107523  
; Sequence 107523, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 107523  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-107523

Query Match 82.2%; Score 14.8; DB 12; Length 25;  
Best Local Similarity 88.9%; Pred. No. 77;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18  
||| ||||| ||||| |||||  
Db 8 CTTTCTAGAAATGCCCG 25

## RESULT 2

US-11-136-527-339204/c  
; Sequence 339204, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 339204  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-339204

Query Match 82.2%; Score 14.8; DB 12; Length 25;  
Best Local Similarity 88.9%; Pred. No. 77;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18  
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Db 23 CTGGCTAGACTGCCCG 6

## RESULT 3

US-10-310-914A-925402/c  
; Sequence 925402, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 925402  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-925402

Query Match 76.7%; Score 13.8; DB 8; Length 22;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCCG 18  
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Db 17 TTTCTAGTACTGCCCG 1

## RESULT 4

US-11-121-849-9721  
; Sequence 9721, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 9721  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-9721

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCCG 18  
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Db 3 TGTCTAACTGCCTAG 19

## RESULT 5

US-11-121-849-297925  
; Sequence 297925, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 297925  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-297925

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCAG 18  
 DB 7 TTCTAGTACTGCCAG 23

RESULT 6  
 US-11-121-849-366615  
 ; Sequence 366615, Application US/11121849  
 ; Publication No. US20050272080A1  
 ; GENERAL INFORMATION:

; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
 ; TITLE OF INVENTION: Microarrays  
 ; FILE REFERENCE: 3684.1  
 ; CURRENT APPLICATION NUMBER: US/11/121,849  
 ; CURRENT FILING DATE: 2005-05-03  
 ; PRIOR APPLICATION NUMBER: 60/567,949  
 ; PRIOR FILING DATE: 2004-05-03  
 ; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 366615  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-366615

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCAG 18  
 DB 6 TGGCTGGAAGTCCAG 22

RESULT 7  
 US-11-136-527-127254  
 ; Sequence 127254, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 673904  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 127254  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Probe  
 US-11-136-527-127254

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCCA 17  
 DB 4 CTGCTCTAGAACTTTCCA 20

# RESULT 8

US-11-136-527-321780/c  
 ; Sequence 321780, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 321780  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Probe  
 US-11-136-527-321780

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCCA 17  
 DB 24 CTGCTGGAAGTCCCA 8

# RESULT 9

US-11-136-527-330649  
 ; Sequence 330649, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 330649  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Probe  
 US-11-136-527-330649

Query Match 76.7%; Score 13.8; DB 12; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCCA 17  
 DB 3 CTGCTCTAGAACTTTCCA 19

# RESULT 10

US-11-175-859-98954  
 ; Sequence 98954, Application US/11175859

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; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US/11/175,859
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98954
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-98954

Query Match          76.7%; Score 13.8; DB 12; Length 50;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCCCA 17
   ||||| |||||
Db 32 CTGTCTACCACTGCCCA 48

RESULT 11
US-10-310-914A-1209005
; Sequence 1209005, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1209005
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1209005

Query Match          74.4%; Score 13.4; DB 8; Length 19;
Best Local Similarity 73.3%; Pred. No. 4.7e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCCA 18
   :||| :|||
Db 5 UCUGAGCCUGCCCA 19

RESULT 12
US-11-101-244-47652
; Sequence 47652, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
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; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 47652
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-47652

Query Match          74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCTAGAACTGCCCA 17
   ||||| :|||
Db 1 GUCAGAGAACUGCCCA 15

RESULT 13
US-11-101-244-365369
; Sequence 365369, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 365369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-365369

Query Match          74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCTAGAACTGCCCA 17
   ||||| :|||
Db 1 GUCAGAGAACUGCCCA 15

RESULT 14
US-11-101-244-978416/c
; Sequence 978416, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
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; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 978416  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-978416

Query Match 74.4%; Score 13.4; DB 10; Length 19;  
 Best Local Similarity 93.3%; Pred. No. 4.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15  
 DB 18 CTGTGTAAGCTGCC 4

RESULT 15  
 US-11-083-784-47652  
 ; Sequence 47652, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 47652  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-47652

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3.GTCTAGAACTGCCCA 17  
 DB 1 GUCCAGAACUGCCCA 15

RESULT 16  
 US-11-083-784-365369  
 ; Sequence 365369, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 365369  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-365369

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCTAGAACTGCCCA 17  
 DB 1 GUCCAGAACUGCCCA 15

RESULT 17  
 US-11-083-784-978416/C  
 ; Sequence 978416, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 978416  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-978416

Query Match 74.4%; Score 13.4; DB 11; Length 19;  
 Best Local Similarity 93.3%; Pred. No. 4.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15  
 DB 18 CTGTGTAAGCTGCC 4

RESULT 18  
 US-10-310-914A-535346  
 ; Sequence 535346, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiller, Kyuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: Patent in version 3.3

; SEQ ID NO 535346  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-535346

Query Match 74.4%; Score 13.4; DB 8; Length 21;  
Best Local Similarity 73.3%; Pred. No. 4.8e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTCCCG 18  
: : ||| : ||| :  
Db 3 UCUGAACUGCCUG 17

## RESULT 19

US-10-310-914A-497795  
; Sequence 497795, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 497795

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-497795

Query Match 74.4%; Score 13.4; DB 8; Length 22;  
Best Local Similarity 73.3%; Pred. No. 4.8e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTCCCG 18  
: : ||| : ||| :  
Db 1 UCUGAACUGCCCG 15

## RESULT 20

US-11-121-849-76084/c  
; Sequence 76084, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 76084

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-11-121-849-76084

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15  
: : ||| : ||| :  
Db 23 CTGTCTAGAACTGCC 9

## RESULT 21

US-11-121-849-76085/c  
; Sequence 76085, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 76085

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-11-121-849-76085

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15  
: : ||| : ||| :  
Db 17 CTGTCTAGAACTGCC 3

## RESULT 22

US-11-121-849-360704/c  
; Sequence 360704, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 360704

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-11-121-849-360704

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15  
: : ||| : ||| :  
Db 18 CTGTCTAGAACTGCC 4

## RESULT 23

US-11-136-527-116504/c  
; Sequence 116504, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:

; APPLICANT: Wveth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294



; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 116504  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-116504

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15  
|||  
DB 19 CTGCTAGAACTGCC 5

## RESULT 24

US-11-136-527-116505/c  
; Sequence 116505, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 116505  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-116505

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15  
|||  
DB 16 CTGCTAGAACTGCC 2

## RESULT 25

US-11-136-527-235336/c  
; Sequence 235336, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 235336  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe

US-11-136-527-235336

Query Match 74.4%; Score 13.4; DB 12; Length 25;  
Best Local Similarity 93.3%; Pred. No. 5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCC 16  
|||  
DB 21 TGTATAGAACTGCC 7

Search completed: March 3, 2006, 07:56.43  
Job time : 98.0559 secs

**This Page Blank (uspto)**

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds  
(without alignments)  
855.220 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 ctgctagaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- EST:\*
- 1: gb\_est1:\*
  - 2: gb\_est2:\*
  - 3: gb\_est3:\*
  - 4: gb\_hic:\*
  - 5: gb\_est4:\*
  - 6: gb\_est5:\*
  - 7: gb\_est6:\*
  - 8: gb\_est7:\*
  - 9: gb\_gse1:\*
  - 10: gb\_gse2:\*
  - 11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	74.4	58	8	DR104908 JHU075B06
2	13.4	74.4	65	5	BU947098 r19b05.y
3	13.2	73.3	61	9	CC591222 CH240.391
4	13.2	73.3	79	1	AI903025 QV-BT022-
5	13.2	73.3	80	1	AJ649674 AJ649674
6	12.8	71.1	68	10	CW156639 104_559.1
7	12.8	71.1	68	10	CW156640 104_559.1
8	12.8	71.1	70	10	BX145365
9	12.8	71.1	71	1	AL794076
10	12.8	71.1	77	1	AA045040
11	12.4	68.9	35	6	CF642114 D47_H04_F
12	12.4	68.9	65	6	CD967875 SEY_37_Ge
13	12.4	68.9	80	11	CR136088
14	12.2	67.8	67	9	BZ594304
15	12.2	67.8	70	1	AA118970
16	12.2	67.8	72	10	CL639237
17	12.2	67.8	73	1	AI941463
18	12.2	67.8	73	1	AL850449
19	12.2	67.8	73	7	CK725727
20	12.2	67.8	73	9	AZ663394
21	12.2	67.8	78	2	BG749927
22	12.2	67.8	78	9	AZ663149

96 11.2 62.2 58 10 AL754659 Arabidops  
c 97 11.2 62.2 61 5 BQ757255 Ebem10 SO  
c 98 11.2 62.2 61 11 CR092757 Forward s  
99 11.2 62.2 62 1 AI801122 t085d12.x  
c 100 11.2 62.2 62 1 AW064193 SP0639 KR

## ALIGNMENTS

RESULT 1  
DR104908  
LOCUS  
DEFINITION JHU075B06L58 Canine cardiovascular system biased cDNA Canis  
familiaris CDNA, mRNA sequence:  
ACCESSION DR104908  
VERSION DR104908.1 GI:67564263  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE 1 (bases 1 to 58)  
AUTHORS DiSilvestre,D., Yung,C., Gao,Z., Farukhi,Y., Winslow,R.L. and  
Tomaseilli,G.F.  
TITLE Canine cardiovascular system biased cDNA sequences  
JOURNAL Unpublished (2005)  
COMMENT Contact: Gordon F. Tomaseilli  
Johns Hopkins University  
720 Rutland Avenue/Ross 844, Baltimore, MD 21205, USA  
Tel: 4109552774  
Fax: 4105022096  
Email: gtomaseil@jhmi.edu.

FEATURES  
source

1. 58  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/strain="Mixed"  
/db\_xref="taxon:9615"  
/sex="Mixed"  
/clone\_lib="Canine cardiovascular system biased cDNA"  
/note="Organ: Mixed; Vector: pCDNA3.1; Site 1: EcoRI;  
Site 2: XhoI; Adult tissue from eye, lung, aorta,  
pulmonary artery and brain; neonatal tissue from liver,  
spleen, thymus, lung, kidney, aorta and brain; 50% is from  
cardiac tissues."

## ORIGIN

Query Match 74.4%; Score 13.4; DB 8; Length 58;  
Best Local Similarity 93.3%; Pred. No. 3.3e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTGAACTGCC 16  
|||||

Db 31 TGCTGAACTGCC 45  
|||||

RESULT 2  
BU947098  
LOCUS  
DEFINITION BU947098 65 bp mRNA linear EST 09-JAN-2003  
r19b05.y1 Meloidogyne hapla J2 SL1 TOPO v1 Meloidogyne hapla cDNA  
s., mRNA sequence.

ACCESSION BU947098  
VERSION BU947098.1 GI:24198163  
KEYWORDS EST.  
SOURCE Meloidogyne hapla

## ORGANISM

Eukaryota; Metazoa; Chromadorea; Nematoda; Tylenchida; Tylenchida;  
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE  
AUTHORS

1 (bases 1 to 65)  
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,

TITLE  
JOURNAL  
COMMENT

Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarelshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone will not be made available due to an unidentified  
microbial contamination of the source material. The library was  
constructed by Claire Murphy and Dr. James McCarter at Washington  
University, St. Louis. J2 were provided by Dr. Valerie Williamson  
of the University of California at Davis  
(vmwilliamson@ucdavis.edu).  
Putative full length read  
The vector to vector length is 75  
Seq primer: -40RP from Gibco.

FEATURES  
source

1. 65  
Location/Qualifiers  
/organism="Meloidogyne hapla"  
/mol\_type="mRNA"  
/db\_xref="taxon:6305"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne hapla J2 SL1 TOPO v1"  
/note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;  
Site 2: EcoRI; The library was constructed by Claire  
Murphy and Dr. James McCarter at Washington University,  
St. Louis. Oligo(dT)-SL1 PCR based library. Meloidogyne  
hapla J2 cDNA PCR products of size >400 nucleotides  
containing SL1 on the 5' end and oligo(dT) on the 3' end  
were non-directionally cloned into pCRII-TOPO(Invitrogen)  
following the Topo TA cloning protocol. J2 were provided  
by Dr. Valerie Williamson of University of California at  
Davis (vmwilliamson@ucdavis.edu)."

## ORIGIN

Query Match 74.4%; Score 13.4; DB 5; Length 65;  
Best Local Similarity 93.3%; Pred. No. 3.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCC 18  
|||||

Db 13 TCTAGAACTGCC 27  
|||||

## RESULT 3

CC591222/c

LOCUS

DEFINITION

CH240\_391K18.TARBAC13P2 CHORI-240 Bos taurus genomic clone

CH240\_391K18, genomic survey sequence.

CC591222

VERSION

CC591222.1 GI:31948692

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 61)

AUTHORS

Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,  
Tsai,M., Cloutier,A., Lee,D., Girm,N., Olson,T., Mayo,M., Chiu,R.,  
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,  
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,  
Schlein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,  
Dalymphe,B.P. and Tellam,R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398



```

ORIGIN

Query Match      73.3%;   Score 13.2;  DB 1;   Length 80;
Best Local Similarity 83.3%;   Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CTGTCCTAGAACTGCCCAG 18
      ||||| ||| ||| |||
Db      17  CTGTCCTAGACCTCCCTAG 34

RESULT 6
LOCUS   CW156639/c
DEFINITION
104_559_11146794.116_36378_069 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11146794, genomic survey
sequence.
ACCESSION   CW156639
VERSION     CW156639.1 GI:54849186
KEYWORDS    GS.
SOURCE      Sorghum bicolor (sorghum)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 68)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holean,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martiniessen,R.A.
TITLE       Sorghum genome sequencing by methylation filtration
JOURNAL     PLoS Biol. 3 (1), e13 (2005)
PUBMED     15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 559 row: 1 column: 18
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 68.
            Location/Qualifiers
                1..68
                /organism="Sorghum bicolor"
                /mol_type="genomic DNA"
                /cultivar="ATx623"
                /db_xref="taxon:4558"
                /clone="11146794"
                /clone_lib="Sorghum methylation filtered library (LibID:
                104)"
                /notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
                prepared from purified nuclei was randomly sheared,
                end-repaired, size fractionated to enrich for the 0.5 to 5
                kb fraction, ligated into HincII-digested pBCSK(-) vector
                and electroporated into E. coli cells. This is a
                methylation filtered library."

FEATURES
source
ORIGIN

Query Match      71.1%;   Score 12.8;  DB 10;   Length 68;
Best Local Similarity 87.5%;   Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  TGTCTAGAACTGCCCA 17
      ||||| ||| ||| |||
Db      54  TGTCTAGAACTCCACA 39

RESULT 7
LOCUS   CW156640
DEFINITION
104_559_11146794.116_36378_069 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11146794, genomic survey
sequence.
ACCESSION   CW156640
VERSION     CW156640.1 GI:54849187
KEYWORDS    GS.
SOURCE      Sorghum bicolor (sorghum)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 68)
AUTHORS    Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holean,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martiniessen,R.A.
TITLE       Sorghum genome sequencing by methylation filtration
JOURNAL     PLoS Biol. 3 (1), e13 (2005)
PUBMED     15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 559 row: 1 column: 18
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 68.
            Location/Qualifiers
                1..68
                /organism="Sorghum bicolor"
                /mol_type="genomic DNA"
                /cultivar="ATx623"
                /db_xref="taxon:4558"
                /clone="11146794"
                /clone_lib="Sorghum methylation filtered library (LibID:
                104)"
                /notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
                prepared from purified nuclei was randomly sheared,
                end-repaired, size fractionated to enrich for the 0.5 to 5
                kb fraction, ligated into HincII-digested pBCSK(-) vector
                and electroporated into E. coli cells. This is a
                methylation filtered library."

FEATURES
source

```

humquery@sanger.ac.uk Unpublished  
This sequence was generated from the T7 end of BAC 106H4. 106H4 is  
part of the Daniokey BAC library created by R. Plasterk and N.V.  
Keygene. Further details:  
http://www.sanger.ac.uk/Projects/D\_reio/.

Location/Qualifiers

1..70  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEY-106H4"  
/tissue\_type="Testis"  
/note="Vector pindigoBAC-536"

## ORIGIN

Query Match 71.1%; Score 12.8; DB 10; Length 70;  
Best Local Similarity 87.5%; Pred. No. 7.2e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCCA 17  
||| ||||| |||||  
Db 64 TGTATAGAACTGCCCA 49

## RESULT 9

AL794076/c  
LOCUS  
DEFINITION AL794076 XGC-neurula Xenopus tropicalis cDNA clone TNeu116a17 5',  
mRNA sequence. EST 13-NOV-2003

ACCESSION AL794076.2 GI:38315956

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)  
Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Silurana.

## REFERENCE

1 (bases 1 to 71)  
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.  
Sanger Xenopus tropicalis EST project 2001 (11\_2003)

## TITLE

Unpublished (2003)

## JOURNAL

On Jun 25, 2002 this sequence version replaced gi:21579780.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dt primed from Sug of poly A+ RNA from neurula.

EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the

5' end and NotI at the 3' end.

Host: pCS107; Site 1: EcoRI; Site 2: NotI

Vector: Escherichia coli DH10B

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TNeu116a17.plcSP6

Sequencing primer: SP6

## FEATURES

source

1..71

Location/Qualifiers

/organism="Xenopus tropicalis"

/mol\_type="mRNA"

/db\_xref="taxon:8364"

/clone="TNeu116a17"

/dev\_stage="neurula"

/lab\_host="Escherichia coli DH10B"

/clone\_lib="XGC-neurula"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA

was oligo dt primed from Sug of poly A+ RNA from neurula.

EcoRI-NotI cut cDNA was then ligated into pCS107 with

EcoRI at the 5' end and NotI at the 3' end."

## ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 71;  
Best Local Similarity 87.5%; Pred. No. 7.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCC 16  
||| ||||| |||||  
Db 44 CTTCCTAGAACTGCC 29

## Matches

14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## Qy

2 TGTCTAGAACTGCCCA 17  
||| ||||| |||||

## Db

67 TGTCTAGAACTGCCCA 52  
||| ||||| |||||

## RESULT 10

AA045040/c

LOCUS

DEFINITION

zk76f10.r1 Soares pregnant uterus\_NbHPU Homo sapiens cDNA clone

IMAGE:488779 5', mRNA sequence.

ACCESSION AA045040

VERSION AA045040.1 GI:1523242

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 77)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.P., Chiapelli,B.,

Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Hawkins,M., Hultman,M., Kucaba,I., Lacy,M., Le,M., Le,N.,

Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,

Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.

and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

8889549

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1819 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 62.

Location/Qualifiers

1..77

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3803366"

/db\_xref="taxon:9606"

/clone="IMAGE:488779"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;

Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dt) primer [5',

AACTGGAAGATTCGCGCGCTTTTCTTTTCTTTT 3',

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

Query Match 71.1%; Score 12.8; DB 1; Length 77;  
Best Local Similarity 87.5%; Pred. No. 7.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

## ORIGIN

Qy 1 CTGTCTAGAACTGCC 16  
||| ||||| |||||  
Db 44 CTTCCTAGAACTGCC 29

```

RESULT 11
LOCUS CF642114/c
DEFINITION D47_H04 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
ACCESSION CF642114
VERSION CF642114.1 GI:37409193
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE 1 (bases 1 to 39)
AUTHORS Nugent, K.G., Choffe, K. and Saville, B.J.
TITLE Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
JOURNAL Fungal Genet. Biol. 41 (3), 349-360 (2004)
PUBMED 14761795
COMMENT Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-047-UTM row: 04 column: H
Seq primer: T7 Reverse (5' GAGTATACGACTCTACTATAGG 3')
High quality sequence stop: 39.
FEATURES
    source
        location/Qualifiers
            1..39
                /organism="Ustilago maydis"
                /mol_type="mRNA"
                /strain="FBD12"
                /db_xref="taxon:5270"
                /cell_type="Mycelia"
                /dev_stage="Filamentous diploid"
                /clone_lib="Filamentous Forced Diploid"
                /note="Vector: pSport; mRNA was extracted from diploid
                mycelia. A cDNA library was constructed and
                unidirectionally cloned into pSPORT plasmid, with the use
                of the Superscript II cDNA Library Construction Kit."
ORIGIN
    Query Match 68.9%; Score 12.4; DB 6; Length 39;
    Best Local Similarity 92.9%; Pred. No. 1.1e+05;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 TCTAGAACTGCCCA 17
Db 33 TCTAGAACTACCCA 20

RESULT 12
LOCUS CD967875
DEFINITION SEV 37 Genetag2 Zea mays cDNA, mRNA sequence.
ACCESSION CD967875
VERSION CD967875.1 GI:32828197
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 65)
AUTHORS Genoplante.
TITLE Unpublished (2003)
JOURNAL
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

```

```

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
    source
        location/Qualifiers
            1..65
                /organism="Zea mays"
                /mol_type="mRNA"
                /cultivar="mixture"
                /db_xref="taxon:4577"
                /clone_lib="Genetag2"
ORIGIN
    Query Match 68.9%; Score 12.4; DB 6; Length 65;
    Best Local Similarity 92.9%; Pred. No. 1.2e+05;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTCTCTAGAACTGC 14
Db 35 CTGTCGAGAACTGC 48

RESULT 13
LOCUS CR136088/c
DEFINITION CR136088 80 bp DNA linear GSS 06-JUL-2004
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHP358e14, genomic survey sequence.
ACCESSION CR136088
VERSION CR136088.1 GI:49883814
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 80)
AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
    source
        location/Qualifiers
            1..80
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /db_xref="taxon:10090"
                /clone="MHP358e14"
                /clone_lib="MHPp"
ORIGIN
    Query Match 68.9%; Score 12.4; DB 11; Length 80;
    Best Local Similarity 92.9%; Pred. No. 1.2e+05;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 TCTAGAACTGCCCA 17
Db 27 TCTATAACTGCCCA 14

RESULT 14
LOCUS BZ594304/c
DEFINITION BZ594304 67 bp DNA linear GSS 07-JAN-2003
SALK_083788.31.75.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_083788.31.75.x, genomic
survey sequence.
ACCESSION BZ594304
VERSION BZ594304.1 GI:27534823
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

```



REFERENCE 1 (bases 1 to 67)  
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 TITLE A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA.  
 Class: TDNA tagged.  
 FEATURES Location/Qualifiers  
 source 1..67  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK 083788.31.75.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
 ORIGIN  
 Query Match 67.8%; Score 12.2; DB 9; Length 67;  
 Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CTGCTAGAACTGCCCA 17  
 ||||| ||||| |||||  
 Db 37 CTGTTTAAAACTGCCCA 21  
 RESULT 15  
 AAl18970/c  
 LOCUS AAl18970.1 67 bp mRNA linear EST 17-FEB-1997  
 DEFINITION mp61h08.r1 Soares thymus 2NBMT Mus musculus cDNA clone IMAGE:573759  
 5' similar to TR:G1166576 G1166576 170 KDA SYNAPTANIN ISOFORM ;,  
 mRNA sequence.  
 ACCESSION AAl18970  
 VERSION AAl18970.1 GI:1676514  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 70)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steproe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mousees@watson.wustl.edu  
 This clone is available royalty-free through LML; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:348407  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 1.  
 FEATURES Location/Qualifiers  
 source 1..70  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:573759"  
 /sex="male"  
 /tissue\_type="Thymus"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares thymus 2NBMT"  
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5'  
 TGTATCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT7T3 vector. RNA  
 provided by Dr. Bertrand Jordan. Library went through two  
 rounds of normalization, and was constructed by Bento  
 Soares and M.Fatima Bonaldo."  
 ORIGIN  
 Query Match 67.8%; Score 12.2; DB 1; Length 70;  
 Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CTGCTAGAACTGCCCA 17  
 ||||| ||||| |||||  
 Db 19 CTTGCAGAACTGCCCA 3  
 RESULT 16  
 LOCUS CL639237  
 DEFINITION CL639237.2 72 bp mRNA linear GSS 22-MAR-2005  
 G084C11 GUTC Gene Trap Library GV07C05 Mus musculus cDNA clone  
 G084C11, mRNA sequence.  
 ACCESSION CL639237  
 VERSION CL639237.2 GI:61684937  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 72)  
 AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,  
 Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.  
 TITLE A large-scale, gene-driven mutagenesis approach for the functional  
 analysis of the mouse genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
 PUBMED 12904583  
 COMMENT On Mar 22, 2005 this sequence version replaced gi:49487684.  
 Contact: GUTC  
 German Genetrap Consortium (GUTC)  
 Email: [info@genetrap.de](mailto:info@genetrap.de)  
 U3CEO gene trap. Sequence tag generated by 5' RACE. Additional  
 sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=G084C11'. ES cell line harboring insertion mutation of  
 target gene is available at:  
 'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
 1' Inhouse Sequence Identifier: 23498  
 Class: Gene Trap.  
 FEATURES Location/Qualifiers  
 source 1..72  
 /organism="Mus musculus"

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/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clones="G084C11"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells (C57BL/6J x 129Sv/SvEvTac) F1"
/clone_lib="GUTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN
Query Match      67.8%; Score 12.2; DB 10; Length 72;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
    ||| ||||| |||
Db 18 CTGGCGAGAACTGGCCA 34

RESULT 17
A1941463
LOCUS      A1941463      73 bp      mRNA      linear      EST 12-JUL-2004
DEFINITION gb90c02.y1 Gm-cl017 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl017-699 5' similar to TR:Q39154 Q39154 MYB-RELATED PROTEIN. ; , mRNA sequence.
ACCESSION  A1941463
VERSION    A1941463.1 GI:5688448
KEYWORDS   EST.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE  1 (bases 1 to 73)
AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvett,V.,
            Khanna,A., Rolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
TITLE     Public Soybean EST Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            When it has been determined, an EST from the other end of this
            clone is listed in the 'Other ESTs on clone' field. Trace
            considered overall poor quality Possible reversed clone: similarity
            on wrong strand This clone is available through: Biogenetic
            Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
            4163; email: info@biogeneticservices.com)
            High quality sequence stop: 1.
            Location/Qualifiers
                1..73
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Williams 82"
                /db_xref="taxon:3847"
                /clone="GENOME SYSTEMS CLONE ID: Gm-cl017-699"
                /tissue_type="vegetable buds of field grown plants"
                /lab_host="XL10-Gold"
                /clone_lib="Gm-cl017"
                /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
                XhoI; This cDNA library was constructed from mRNA isolated
                from vegetable buds of field grown plants. The cDNA
                library was prepared using the Stratagene pBluescript II
                XR library construction kit. Complementary DNA was

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synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelting."

ORIGIN
Query Match      67.8%; Score 12.2; DB 1; Length 73;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCAG 18
    ||| ||||| |||
Db 42 TGCTAGAACTGGCAAG 58

RESULT 18
AL850449
LOCUS      AL850449      73 bp      mRNA      linear      EST 26-NOV-2003
DEFINITION AL850449 XGC-egg Xenopus tropicalis cDNA clone TEG909110 5', mRNA
            sequence.
ACCESSION  AL850449
VERSION    AL850449.2 GI:38561596
KEYWORDS   EST.
SOURCE     Xenopus tropicalis (western clawed frog)
ORGANISM   Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE  1 (bases 1 to 73)
AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL   Unpublished (2003)
COMMENT   On Sep 15, 2002 this sequence version replaced gi:22870671.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE ID: TEG909110.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
            Location/Qualifiers
                1..73
                /organism="Xenopus tropicalis"
                /mol_type="mRNA"
                /db_xref="taxon:8364"
                /clone="TEG909110"
                /dev_stage="egg"
                /lab_host="Escherichia coli XL1-blue"
                /clone_lib="XGC-egg"
                /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                was oligo dt primed from Sug of poly A+ RNA from egg.
                EcoRI-NotI cut cDNA was then ligated into pCS107 with
                EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      67.8%; Score 12.2; DB 1; Length 73;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
    ||| ||||| |||

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24 CTTGTTTATAACTGCCCTA 40

Db

RESULT 19  
CK725727/c  
LOCUS  
DEFINITION  
Wucheria bancrofti L3 cDNA (SAW96MLW-WBL3)  
Wucheria bancrofti cDNA clone SWBBL3CAW03G08 5', mRNA sequence.  
CK725727  
CK725727.1 GI:42579265  
EST.  
Wucheria bancrofti  
Wucheria bancrofti  
Wucheria bancrofti  
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Wuchereria.  
1 (bases 1 to 73)  
Williams,S.A.  
Genes Expressed in L3 infective stage larvae of Wuchereria  
bancrofti  
Unpublished (1999)  
Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genome@smith.edu  
Seq primer: pBluescript SK.  
Location/Qualifiers  
1..73  
/organism="Wuchereria bancrofti"  
/mol\_type="mRNA"  
/db\_xref="taxon:6293"  
/clone="SWBBL3CAW03G08"  
/dev\_stage="L3 infective stage larvae"  
/lab\_host="XLI-Blue MRP"  
/clone\_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Lymphatic filarial nematode parasite of humans.  
mRNA was prepared from approximately 8,000 L3 isolated  
from mosquitoes in Cairo, Egypt and converted to  
double-stranded cDNA using reverse transcriptase and  
oligo(dT) followed by RNase H and DNA pol I. The library  
has 1.0 x 10E6 independent recombinants and the average  
insert size is ~900 bp. The library was constructed by  
Michelle. Lizotte-Waniewski. The library is available  
from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN

Query Match 67.8%; Score 12.2; DB 7; Length 73;  
Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCCG 18  
|||||  
Db 51 TGTCTATAAATGTCAC 35

RESULT 20  
A2663994/c  
LOCUS  
DEFINITION  
1M0543M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0543M20 R, genomic survey sequence.  
A2663994  
A2663994.1 GI:11801140  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 73)

REFERENCE 1

AUTHORS

TITLE

JOURNAL

COMMENT

ORGANISM

Wucheria bancrofti

Wucheria bancrofti

Wucheria bancrofti

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Wuchereria.  
1 (bases 1 to 73)  
Williams,S.A.  
Genes Expressed in L3 infective stage larvae of Wuchereria  
bancrofti  
Unpublished (1999)  
Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genome@smith.edu  
Seq primer: pBluescript SK.  
Location/Qualifiers  
1..73  
/organism="Wuchereria bancrofti"  
/mol\_type="mRNA"  
/db\_xref="taxon:6293"  
/clone="SWBBL3CAW03G08"  
/dev\_stage="L3 infective stage larvae"  
/lab\_host="XLI-Blue MRP"  
/clone\_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Lymphatic filarial nematode parasite of humans.  
mRNA was prepared from approximately 8,000 L3 isolated  
from mosquitoes in Cairo, Egypt and converted to  
double-stranded cDNA using reverse transcriptase and  
oligo(dT) followed by RNase H and DNA pol I. The library  
has 1.0 x 10E6 independent recombinants and the average  
insert size is ~900 bp. The library was constructed by  
Michelle. Lizotte-Waniewski. The library is available  
from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN

Query Match 67.8%; Score 12.2; DB 7; Length 73;  
Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCCG 18  
|||||  
Db 51 TGTCTATAAATGTCAC 35

RESULT 20  
A2663994/c  
LOCUS  
DEFINITION  
1M0543M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0543M20 R, genomic survey sequence.  
A2663994  
A2663994.1 GI:11801140  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 73)

REFERENCE 1

AUTHORS

TITLE

JOURNAL

COMMENT

ORGANISM

Wucheria bancrofti

Wucheria bancrofti

Wucheria bancrofti

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Wuchereria.  
1 (bases 1 to 73)  
Williams,S.A.  
Genes Expressed in L3 infective stage larvae of Wuchereria  
bancrofti  
Unpublished (1999)  
Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genome@smith.edu  
Seq primer: pBluescript SK.  
Location/Qualifiers  
1..73  
/organism="Wuchereria bancrofti"  
/mol\_type="mRNA"  
/db\_xref="taxon:6293"  
/clone="SWBBL3CAW03G08"  
/dev\_stage="L3 infective stage larvae"  
/lab\_host="XLI-Blue MRP"  
/clone\_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Lymphatic filarial nematode parasite of humans.  
mRNA was prepared from approximately 8,000 L3 isolated  
from mosquitoes in Cairo, Egypt and converted to  
double-stranded cDNA using reverse transcriptase and  
oligo(dT) followed by RNase H and DNA pol I. The library  
has 1.0 x 10E6 independent recombinants and the average  
insert size is ~900 bp. The library was constructed by  
Michelle. Lizotte-Waniewski. The library is available  
from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN

Query Match 67.8%; Score 12.2; DB 7; Length 73;  
Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCCG 18  
|||||  
Db 51 TGTCTATAAATGTCAC 35

RESULT 20  
A2663994/c  
LOCUS  
DEFINITION  
1M0543M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0543M20 R, genomic survey sequence.  
A2663994  
A2663994.1 GI:11801140  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 73)

REFERENCE 1

AUTHORS

TITLE

JOURNAL

COMMENT

ORGANISM

Wucheria bancrofti

Wucheria bancrofti

Wucheria bancrofti

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Wuchereria.  
1 (bases 1 to 73)  
Williams,S.A.  
Genes Expressed in L3 infective stage larvae of Wuchereria  
bancrofti  
Unpublished (1999)  
Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genome@smith.edu  
Seq primer: pBluescript SK.  
Location/Qualifiers  
1..73  
/organism="Wuchereria bancrofti"  
/mol\_type="mRNA"  
/db\_xref="taxon:6293"  
/clone="SWBBL3CAW03G08"  
/dev\_stage="L3 infective stage larvae"  
/lab\_host="XLI-Blue MRP"  
/clone\_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Lymphatic filarial nematode parasite of humans.  
mRNA was prepared from approximately 8,000 L3 isolated  
from mosquitoes in Cairo, Egypt and converted to  
double-stranded cDNA using reverse transcriptase and  
oligo(dT) followed by RNase H and DNA pol I. The library  
has 1.0 x 10E6 independent recombinants and the average  
insert size is ~900 bp. The library was constructed by  
Michelle. Lizotte-Waniewski. The library is available  
from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN

Query Match 67.8%; Score 12.2; DB 7; Length 73;  
Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCCG 18  
|||||  
Db 51 TGTCTATAAATGTCAC 35

RESULT 20  
A2663994/c  
LOCUS  
DEFINITION  
1M0543M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0543M20 R, genomic survey sequence.  
A2663994  
A2663994.1 GI:11801140  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 73)

REFERENCE 1

AUTHORS

TITLE

JOURNAL

COMMENT

ORGANISM

Wucheria bancrofti

Wucheria bancrofti

Wucheria bancrofti

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Wuchereria.  
1 (bases 1 to 73)  
Williams,S.A.  
Genes Expressed in L3 infective stage larvae of Wuchereria  
bancrofti  
Unpublished (1999)  
Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 4135853826  
Fax: 4135853786  
Email: genome@smith.edu  
Seq primer: pBluescript SK.  
Location/Qualifiers  
1..73  
/organism="Wuchereria bancrofti"  
/mol\_type="mRNA"  
/db\_xref="taxon:6293"<

REFERENCE 1 (bases 1 to 78)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsb-r@mail.nih.gov](mailto:cgapsb-r@mail.nih.gov)  
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: L1CM1684 row: g column: 17  
 High quality sequence stop: 78.

## FEATURES

source

1. .78  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4845352"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 43"  
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAAGGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library. |"

## ORIGIN

Query Match 67.8%; Score 12.2; DB 2; Length 78;  
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCTAGAACTGCCAC 18

||||| ||||| |||||

Db 32 TGCTGGAAGTGCAC 16

## RESULT 22

AZ663149  
 LOCUS AZ663149 78 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M0542E07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0542E07 R, genomic survey sequence.

ACCESSION AZ663149.1 GI:11800295

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 78)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0542 row: E column: 07  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 78.

## FEATURES

source

Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0542E07"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (GI:4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 67.8%; Score 12.2; DB 9; Length 78;  
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCTAGAACTGCCAC 18

||||| ||||| |||||

Db 28 TGCTATTACTGCCTAG 44

## RESULT 23

BG868495/c

LOCUS

DEFINITION 602785880F1 NCI\_CGAP\_SG2 Mus musculus cDNA clone IMAGE:4912002 5',  
 mRNA sequence.

ACCESSION BG868495

VERSION BG868495.1 GI:14219035

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 80)  
 NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsb-r@mail.nih.gov](mailto:cgapsb-r@mail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM10814 row: p column: 19  
 High quality sequence stop: 52.

## FEATURES

Location/Qualifiers

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/mol_type="mRNA"
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/db_xref="taxon:10090"
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/lab_host="DHL0B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
/notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 67.8%; Score 12.2; DB 2; Length 80;
Best Local Similarity 82.4%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCCA 17
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Db 46 CTGCGCTAGAACACCCCA 30

RESULT 24
BH608861
LOCUS 15f21 LL18NC02-trapped exons Homo sapiens genomic clone 15f21,
DEFINITION 76 bp DNA linear GSS 11-AUG-2003
GENOMIC SURVEY SEQUENCE.
ACCESSION BH608861
VERSION BH608861.1 GI:27437317
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 76)
AUTHORS Chen,H., Wang,N., Huo,Y., Sklar,P., MacKinnon,D.F., Potash,J.B.,
McMahon,F.J., Antonarakis,S.E., DePaulo,J.R. Jr, Ross,C.A. and
McInnis,M.G.
TITLE Trapping and sequence analysis of 1138 putative exons from human
chromosome 18
JOURNAL Mol. Psychiatry 8 (6), 619-623 (2003)
PUBMED 12851638
COMMENT Contact: Haiming Chen
Department of Psychiatry
Johns Hopkins University School of Medicine
600 N. Wolfe Street, MD 21287-7463, USA
Tel: 410 614 1530
Fax: 410 614 4728
Email: hc@jhmi.edu
Class: exon-trapped.
FEATURES
Location/Qualifiers
source 1..76
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="15f21"
/clone_lib="LL18NC02-trapped exons"

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Query Match 66.7%; Score 12; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACT 12
   ||| ||||| |||
Db 5 CTGCTCTAGAACT 16

RESULT 25
BJ034925/c
LOCUS 77 bp mRNA linear EST 26-SEP-2003

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DEFINITION BJ034925 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL031f09 5', mRNA sequence.
ACCESSION BJ034925
VERSION BJ034925.1 GI:17396669
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 77)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
Kohara,I.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
FEATURES
Location/Qualifiers
source 1..77
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL031f09"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"

ORIGIN
Query Match 66.7%; Score 12; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCC 15
   ||| ||||| |||
Db 20 TCTAGAACTGCC 9

Search completed: March 3, 2006, 11:01:29
JOB time : 989.737 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds  
(without alignments)  
2714.499 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18

Sequence: 1 tgccttgagaacttcggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl:

1: gb\_da.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	13.8	76.7	20	6	AR366674 Sequence
C 2	13.2	73.3	29	6	E07880 PCR primer
C 3	13.2	73.3	51	6	Q0002237 Sequence
C 4	13.2	73.3	51	6	AR444282 Sequence
C 5	13.2	73.3	51	6	AR444283 Sequence
C 6	13.2	73.3	65	6	Q0555558 Sequence
C 7	13.2	73.3	69	8	AF189371 Homo sapi
C 8	13	72.2	65	6	Q0554821 Sequence
C 9	12.8	71.1	24	6	AX447262 Sequence
C 10	12.4	68.9	22	6	AR492436 Sequence
C 11	12.4	68.9	31	6	AX249088 Sequence
C 12	12.4	68.9	32	6	AR104789 Sequence
C 13	12.4	68.9	38	6	AX220481 Sequence
C 14	12.4	68.9	38	6	AX425282 Sequence
C 15	12.4	68.9	39	6	I34472 Sequence
C 16	12.4	68.9	60	6	Q0538517 Sequence
C 17	12.4	68.9	60	6	Q0542067 Sequence
C 18	12.4	68.9	60	6	Q0547296 Sequence

19	12.4	68.9	68	6	I13480
C 20	12.4	68.9	80	6	BD074975
C 21	12.4	68.9	80	6	AR210850 Sequence
C 22	12.4	68.9	80	6	AR428218 Sequence
C 23	12.4	68.9	80	6	AR584458 Sequence
C 24	12.2	67.8	27	6	AX813491 Sequence
C 25	12.2	67.8	28	6	BD237704 Sequence
C 26	12.2	67.8	28	6	AX278222 Sequence
C 27	12.2	67.8	36	6	AR060746 Sequence
C 28	12.2	67.8	36	6	AX611150 Sequence
C 29	12.2	67.8	50	6	AR393439 Sequence
C 30	12.2	67.8	51	6	AX115865 Sequence
C 31	12.2	67.8	51	6	AX199214 Sequence
C 32	12.2	67.8	60	6	CQ542005 Sequence
C 33	12.2	67.8	60	6	CQ544069 Sequence
C 34	12.2	67.8	60	6	CQ548009 Sequence
C 35	12.2	67.8	60	6	CQ561846 Sequence
C 36	12.2	67.8	60	6	AR393440 Sequence
C 37	12.2	67.8	65	6	CQ556854 Sequence
C 38	12.2	67.8	65	6	CQ558504 Sequence
C 39	12	66.7	20	6	AR649203 Sequence
C 40	12	66.7	36	6	AR337977 Sequence
C 41	12	66.7	38	6	AR336109 Sequence
C 42	12	66.7	51	6	CQ004183 Sequence
C 43	12	66.7	61	6	CQ919690 Sequence
C 44	11.8	65.6	17	6	BD199011 Method an
C 45	11.8	65.6	17	6	BD199012 Method an
C 46	11.8	65.6	18	6	E63218 NAIP transg
C 47	11.8	65.6	19	6	AX840264 Sequence
C 48	11.8	65.6	20	6	A01587 Oligonucleo
C 49	11.8	65.6	20	6	A03836 Nucleotide
C 50	11.8	65.6	20	6	A10446 Synthetic n
C 51	11.8	65.6	20	6	A78920 Sequence 18
C 52	11.8	65.6	20	6	BD190250 Method fo
C 53	11.8	65.6	20	6	I27212 Sequence 18
C 54	11.8	65.6	20	6	I63095 Sequence 18
C 55	11.8	65.6	20	6	AR312197 Sequence
C 56	11.8	65.6	21	6	AX662813 Sequence
C 57	11.8	65.6	21	6	AR528869 Sequence
C 58	11.8	65.6	21	6	AX094894 Sequence
C 59	11.8	65.6	24	6	AR156602 Sequence
C 60	11.8	65.6	24	6	BD221710 Process f
C 61	11.8	65.6	24	6	BD261665 Method of
C 62	11.8	65.6	24	6	AR216734 Sequence
C 63	11.8	65.6	24	6	AR473813 Sequence
C 64	11.8	65.6	24	6	AR482295 Sequence
C 65	11.8	65.6	25	6	A45599 Sequence 4
C 66	11.8	65.6	25	6	AR082280 Sequence
C 67	11.8	65.6	25	6	AR082303 Sequence
C 68	11.8	65.6	25	6	AR120822 Sequence
C 69	11.8	65.6	25	6	AR120845 Sequence
C 70	11.8	65.6	25	6	CQ876140 Sequence
C 71	11.8	65.6	25	6	I12721 Sequence 19
C 72	11.8	65.6	25	6	I12722 Sequence 20
C 73	11.8	65.6	25	6	I78326 Sequence 12
C 74	11.8	65.6	25	6	I78349 Sequence 14
C 75	11.8	65.6	25	6	BD022730 Mammary c
C 76	11.8	65.6	27	6	A22395 primer DNA
C 77	11.8	65.6	27	6	AR146226 Sequence
C 78	11.8	65.6	27	6	AX067186 Sequence
C 79	11.8	65.6	29	6	A44164 Sequence 7
C 80	11.8	65.6	29	6	BD192229 Secreted
C 81	11.8	65.6	30	6	CQ972003 Sequence
C 82	11.8	65.6	30	6	E32668 Peptide inh
C 83	11.8	65.6	30	6	E32673 Peptide inh
C 84	11.8	65.6	31	6	CQ877214 Sequence
C 85	11.8	65.6	34	6	A58326 Sequence 4
C 86	11.8	65.6	34	6	A92326 Sequence 6
C 87	11.8	65.6	34	6	AR105324 Sequence
C 88	11.8	65.6	34	6	AX337942 Sequence
C 89	11.8	65.6	36	6	BD009958 Retrovira
C 90	11.8	65.6	36	6	A58325 Sequence 3
C 91	11.8	65.6	36	6	A63212 Sequence 10

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92 11.8 65.6 36 6 A92325 Sequence 5
93 11.8 65.6 36 6 AR105323 Sequence
c 94 11.8 65.6 36 6 CS078212 Sequence
c 95 11.8 65.6 36 6 CS114690 Sequence
96 11.8 65.6 36 6 AR257264 Sequence
97 11.8 65.6 36 6 AR590072 Sequence
98 11.8 65.6 36 6 AR592969 Sequence
99 11.8 65.6 36 6 AR594390 Sequence
100 11.8 65.6 36 6 AX076720 Sequence

ALIGNMENTS

RESULT 1
AR366674/c
LOCUS AR366674 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 36 from patent US 6329203.
ACCESSION AR366674
VERSION AR366674.1 GI:34599266
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Wyatt,J.
TITLE Antisense modulation of glioma-associated oncogene-1 expression
JOURNAL Patent: US 6329203-A 36 11-DEC-2001;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGGG 18
Db 18 GCCTTGAGAACTTCAGG 2

RESULT 2
E07880/c
LOCUS E07880 29 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer for gaining part of surface antigen protein of Japanese
encephalitis virus.
ACCESSION E07880
VERSION E07880.1 GI:2176012
KEYWORDS JP 1994205672-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS Sato,T., Takamura,C., Yasuda,A., Kamogawa,K. and Yasui,K.
TITLE PRODUCTION OF CHIMERAL PROTEIN HAVING ANTIGEN SITE OF SURFACE
ANTIGEN PROTEIN OF JAPANESE ENCEPHALITIS VIRUS AND HEPATITIS B
JOURNAL VIRUS AND RECOMBINANT BACULOVIRUS THEREFOR
Patent: JP 1994205672-A 2 26-JUL-1994;
NIPPON ZEON CO LTD, TOKYO MET GOV SHINKAI KAGAKU SOGO KENKYUSHO
COMMENT OS None
OC Artificial sequences.
PN JP 1994205672-A/2
PD 26-JUL-1994
PF 19-MAR-1992 JP 1992063699
PI SATO TAKANORI, TAKAMURA CHIZUKO, YASUDA ATSUSHI, PI KAMOGAWA
KOICHI,
PI YASUI KOTARO
PC C12N7/01,A61K39/155,A61K39/29,A61K39/295,C12N15/62,C12N15/86,
PC C12P21/02,
PC (C12N15/62,C12R1.92),(C12P21/02,C12R1.91);

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CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
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FT misc_feature 1..29 /organism='Artificial sequences' FT
FT /note='PCR primer named P-R3L'.
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 7.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGGG 18
Db 18 TGCCTTGAGAACTTCGAG 1

RESULT 3
CQ002237
LOCUS CQ002237 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 877 from Patent WO0147944.
ACCESSION CQ002237
VERSION CQ002237.1 GI:41008869
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 877 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
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ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 51;
Best Local Similarity 83.3%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGGG 18
Db 25 TGCCTTGAGAACTTCGGG 42

RESULT 4
AR444282
LOCUS AR444282 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 693 from patent US 6670464.
ACCESSION AR444282
VERSION AR444282.1 GI:42672061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.

```



TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: US 6670464-A 693 30-DEC-2003;  
Curagen Corporation; New Haven, CT

FEATURES  
source

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/organism="unknown"  
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ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 51;  
Best Local Similarity 83.3%; Pred. No. 7.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
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Db 33 TGCTTAGAGACCTTCGGG 50

RESULT 5

AR444283

LOCUS

DEFINITION Sequence 694 from patent US 6670464. linear PAT 20-FEB-2004

ACCESSION AR444283

VERSION AR444283.1 GI:42672062

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 51)

AUTHORS Shimkete,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: US 6670464-A 694 30-DEC-2003;  
Curagen Corporation; New Haven, CT

FEATURES  
source

1..51  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 51;  
Best Local Similarity 83.3%; Pred. No. 7.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
||||| ||||| ||||| |||||

Db 33 TGCTTAGAGACCTTCGGG 50

RESULT 6

CQ555558

LOCUS

DEFINITION Sequence 25193 from Patent WO0210449. linear PAT 30-JAN-2004

ACCESSION CQ555558

VERSION CQ555558.1 GI:41521985

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.

TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome

JOURNAL Patent: WO 0210449-A 25193 07-FEB-2002;

CompuGen Inc. (US)

FEATURES

1..65  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
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ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 65;  
Best Local Similarity 83.3%; Pred. No. 7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
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Db 3 TGCCTTCAGTACTTCGTG 20

RESULT 7

AF189371

LOCUS

DEFINITION Homo sapiens clone B31U T-cell receptor beta chain (TCRBV20S1) 69 bp mRNA linear PRI 01-FEB-2000

ACCESSION AF189371

VERSION AF189371.1 GI:6841609

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo

REFERENCE 1 (bases 1 to 69)

AUTHORS Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U.,

TITLE Transient T cell receptor beta-chain variable region-specific

expansions of CD4+ and CD8+ T cells during the early phase of  
pediatric human immunodeficiency virus infection: characterization  
of expanded cell populations by T cell receptor phenotyping  
J. Infect. Dis. 181 (1), 107-120 (2000)

JOURNAL PUBMED 10608757

REFERENCE 2 (bases 1 to 69)

AUTHORS Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U.,

Ringuette,N., Samson,J., Lapointe,N. and Sekaly,R.P.

TITLE Direct Submission

JOURNAL Submitted (24-SEP-1999) Laboratoire d'immunologie, IRCM, 110 avenue  
Des Pins ouest, Montreal, Quebec H2W 1R7, Canada

FEATURES

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1..69  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="B31U"  
<1..>69  
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/translation="LLSDSGFYLCAWSGRTYEQYF"

gene

CDS

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Query Match 73.3%; Score 13.2; DB 8; Length 69;  
Best Local Similarity 83.3%; Pred. No. 7e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
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Db 30 TGCTTGAGTACTTCAGG 47

RESULT 8

CQ554821

LOCUS

DEFINITION Sequence 24456 from Patent WO0210449. 65 bp DNA linear PAT 30-JAN-2004

ACCESSION CQ554821

VERSION CQ554821.1 GI:41521248

KEYWORDS

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.  
TITLE Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
JOURNAL Patent: WO 0210449-A 24456 07-FEB-2002;  
CompuGen Inc. (US)  
FEATURES  
source 1. .65  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 65;  
Best Local Similarity 100.0%; Pred. No. 9e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGAGAACTTCGG 18  
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Db 10 TGAGAACTTCGG 22

RESULT 9  
LOCUS AX447262 24 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 3717 from Patent WO0216649.  
ACCESSION AX447262  
VERSION AX447262.1 GI:21696161  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Gunderson,K.  
TITLE Probes and decoder oligonucleotides  
JOURNAL Patent: WO 0216649-A 3717 28-FEB-2002;  
Illumina, Inc. (US)  
FEATURES  
source 1. .24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Computer Generated Probe Sequence."

ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCG 16  
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Db 23 TGCTTAGATCTTCG 8

RESULT 10  
LOCUS AR492436 22 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 5 from patent US 6716813.  
ACCESSION AR492436  
VERSION AR492436.1 GI:47261588  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Lim,D.J., Lee,H.-Y., Webster,P., Andalibi,A., Li,J.-D. and Ganz,T.  
TITLE Use of antimicrobial proteins and peptides for the treatment of  
otitis media and paranasal sinusitis

JOURNAL Patent: US 6716813-A 5 06-APR-2004;  
House Ear Institute; Los Angeles, CA  
FEATURES  
source 1. .22  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 68.9%; Score 12.4; DB 6; Length 22;  
Best Local Similarity 92.9%; Pred. No. 2e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTC 15  
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Db 2 GCCATGAGAACTTC 15

RESULT 11  
LOCUS AX249088/c 31 bp DNA linear PAT 28-SEP-2001  
DEFINITION Sequence 1167 from Patent WO0166800.  
ACCESSION AX249088  
VERSION AX249088.1 GI:15863711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0166800-A 1167 13-SEP-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
FEATURES  
source 1. .31  
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/db\_xref="taxon:9606"

ORIGIN  
Query Match 68.9%; Score 12.4; DB 6; Length 31;  
Best Local Similarity 81.2%; Pred. No. 2e+05;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCG 17  
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Db 29 GTCTTGAGAACTTYG 14

RESULT 12  
LOCUS AR104789/c 32 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 86 from patent US 6093811.  
ACCESSION AR104789  
VERSION AR104789.1 GI:12817497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 32)  
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.  
TITLE Oligonucleotide modulation of cell adhesion  
JOURNAL Patent: US 6093811-A 86 25-JUL-2000;  
FEATURES  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 68.9%; Score 12.4; DB 6; Length 32;  
Best Local Similarity 92.9%; Pred. No. 2e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4 CTTGAGAACTCGG 17
Db 31 CTTGAGAACTCAG 18

RESULT 13
AX220481/c
LOCUS AX220481 38 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5923 from Patent WO0159103.
ACCESSION AX220481
VERSION AX220481.1 GI:15548205
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1..38
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14
Db 37 TGCCTTGAGAACTT 24

RESULT 14
AX425282/c
LOCUS AX425282 38 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 3618 from Patent WO0188124.
ACCESSION AX425282
VERSION AX425282.1 GI:21528664
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1..38
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14
Db 37 TGCCTTGAGAACTT 24

RESULT 15
I34472
LOCUS I34472 39 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 11 from patent US 5597908.
ACCESSION I34472
VERSION I34472.1 GI:1825263
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Taddei-Peters, W.C. and Butler, S.M.
TITLE Immunoreactive peptides of apo(a)
JOURNAL Patent: US 5597908-A 11 28-JAN-1997;
FEATURES
source 1..39
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/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
Db 25 GCCTTGAGAACTTC 12

RESULT 16
CQ538517
LOCUS CQ538517 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 8152 from Patent WO0210449.
ACCESSION CQ538517
VERSION CQ538517.1 GI:41504781
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8152 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTGAGAACTTCGG 18
Db 29 TTGAGAACTTCGG 42

RESULT 17
CQ542067
LOCUS CQ542067 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 11702 from Patent WO0210449.
ACCESSION CQ542067
VERSION CQ542067.1 GI:41508331
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8152 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source 1..60
/organism="Homo sapiens"
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/db_xref="taxon:9606"

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Query Match 68.9%; Score 12.4; DB 6; Length 60;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTGAGAACTTCGG 18
Db 29 TTGAGAACTTCGG 42
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
 1  
 Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
 Oligonucleotide library for detecting rna transcripts and splice  
 variants that populate a transcriptome  
 Patent: WO 0210449-A 11702 07-FEB-2002;  
 CompuGen Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..60  
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 Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
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 Qy 3 CCTTGAGAACTTCG 16  
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 Db 25 CCTTGAGAACTTCG 38  
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 RESULT 18  
 LOCUS CQ547296 60 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 16931 from Patent WO0210449.  
 ACCESSION CQ547296  
 VERSION CQ547296.1 GI:41513560  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
 1  
 Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
 Oligonucleotide library for detecting rna transcripts and splice  
 variants that populate a transcriptome  
 Patent: WO 0210449-A 16931 07-FEB-2002;  
 CompuGen Inc. (US)  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
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 Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
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 Db 3 GCCTTGAGAACTTC 16  
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 RESULT 19  
 LOCUS I13480 68 bp DNA linear PAT 26-JUL-1995  
 DEFINITION Sequence 14 from patent US 5436391.  
 ACCESSION I13480  
 VERSION I13480.1 GI:910821  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 68)  
 Fujimoto, H., Ito, K., Yamamoto, M. and Shimamoto, K.  
 Synthetic insecticidal gene, plants of the genus *oryza* transformed  
 with the gene, and production thereof  
 Patent: US 5436391-A 14 25-JUL-1995;  
 JOURNAL

FEATURES source 1..68  
 /organism="unknown"  
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 ORIGIN  
 Query Match 68.9%; Score 12.4; DB 6; Length 68;  
 Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 CCTTGAGAACTTCG 16  
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 Db 21 CCTCGAGAACTTCG 34  
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 RESULT 20  
 LOCUS BD074975/c 80 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Microbial gene of secreted beta-glucuronidase, gene product, and  
 utilization thereof.  
 ACCESSION BD074975  
 VERSION BD074975.1 GI:22620578  
 KEYWORDS JP 2001515724-A/51.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences: artificial sequences.  
 1 (bases 1 to 80)  
 Jefferson, R.A., Kilian, A. and Keese, P.K.  
 Microbial gene of secreted beta-glucuronidase, gene product, and  
 utilization thereof  
 Patent: JP 2001515724-A 51 25-SEP-2001;  
 CAMBIA BIOSYSTEMS LLC  
 OS Artificial Sequence  
 EN JP 2001515724-A/51  
 PD 25-SEP-2001  
 PF 09-SEP-1998 JP 2000510870  
 PR 09-SEP-1997 US 60/058263  
 PI RICHARD A. JEFFERSON, ANDRZEJ KILIAN, PAUL KONRAD KEESE, PC  
 C12N15/09, A01H5/00, A01K67/027, C12N1/15, C12N1/19, C12N1/21 PC  
 , C12N5/10, C12N5/10,  
 PC C12N9/24, C12Q1/02, G01N33/52// (C12N15/09, C12R1/07), (C12N15/09,  
 PC C12R1/19),  
 PC (C12Q1/02, C12R1/07), C12N15/00, C12N5/00, C12N5/00, (C12N15/00, PC  
 C12R1/07),  
 PC (C12N15/00, C12R1/19)  
 CC Description of Artificial Sequence: Oligonucleotide. CC  
 Product of Synthesis to Overlap and create fragments of CC  
 engineered  
 CC secrettable microbial GUS (Figure 13)  
 FH Key Location/Qualifiers  
 FT source 1..80  
 FT /organism='Artificial Sequence'.  
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 /db\_xref="taxon:32630"  
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 Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 TTGAGAACTTCGGG 18  
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 Db 48 TTGAGAACTTCGTG 35  
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 RESULT 21  
 LOCUS AR210850/c 80 bp DNA linear PAT 20-JUN-2002  
 DEFINITION Sequence 59 from patent US 6391547.  
 ACCESSION AR210850

VERSION AR210850.1 GI:21513688  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS Jefferson, R.A., Harcourt, R. Louise., Kilian, A., Wilson, K. Joanna. and Keese, P. Konrad.  
TITLE Microbial .beta.-glucuronidase genes, gene products and uses thereof  
JOURNAL Patent: US 6391547-A 59 21-MAY-2002;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 68.9%; Score 12.4; DB 6; Length 80;  
Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 TTGAGAACTTCGGG 18  
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Db 48 TTGAGAACTTCGTG 35  
RESULT 22  
AR428218/c  
LOCUS AR428218 80 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 98 from patent US 6641996.  
ACCESSION AR428218  
VERSION AR428218.1 GI:40187611  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 80)  
AUTHORS Jefferson, R.A. and Mayer, J.E.  
TITLE Microbial .beta.-glucuronidase genes, gene products and uses thereof  
JOURNAL Patent: US 6641996-A 98 04-NOV-2003;  
Cambria; ACT;  
AUX;  
FEATURES Location/Qualifiers  
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Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
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QY 5 TTGAGAACTTCGGG 18  
|||||  
Db 48 TTGAGAACTTCGTG 35  
RESULT 23  
AR584458  
LOCUS AR584458 20 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 57 from patent US 6797475.  
ACCESSION AR584458  
VERSION AR584458.1 GI:56625641  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Barnes, G. and Meyer, J.  
TITLE Detection of polymorphisms in the human 5-lipoxygenase gene  
JOURNAL Patent: US 6797475-A 57 28-SEP-2004;  
Millennium Pharmaceuticals, Inc.; Cambridge, MA

FEATURES Location/Qualifiers  
source 1..20  
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ORIGIN  
Query Match 67.8%; Score 12.2; DB 6; Length 20;  
Best Local Similarity 82.4%; Pred. No. 2.6e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GCCTTGAGAACTTCGGG 18  
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Db 3 GCACTGAGAACTTCGGG 19  
RESULT 24  
AX813491  
LOCUS AX813491 27 bp DNA linear PAT 02-DEC-2003  
DEFINITION Sequence 13 from Patent WO03062276.  
ACCESSION AX813491  
VERSION AX813491.1 GI:38636020  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ross, R., Artymluk, P. and Savers, J.  
TITLE Multimers of receptor-binding ligands  
JOURNAL Patent: WO 03062276-A 13 31-JUL-2003;  
Asterion Limited (GB)  
FEATURES Location/Qualifiers  
source 1..27  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
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Best Local Similarity 82.4%; Pred. No. 2.6e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TGCCTTGAGAACTTCGG 17  
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Db 3 TGCCTCGAGGAATTCGG 19  
RESULT 25  
BD237704/c  
LOCUS BD237704 28 bp DNA linear PAT 17-JUL-2003  
DEFINITION Therapeutically active proteins in plants.  
ACCESSION BD237704  
VERSION BD237704.1 GI:33047474  
KEYWORDS JP 2002526116-A/33.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Heifetz, P.B., Goff, S.A., Tuttle, A.B. and Wenk, M.E.G.  
TITLE Therapeutically active proteins in plants  
JOURNAL Patent: JP 2002526116-A 33 20-AUG-2002;  
SYNGENTA PARTICIPATIONS AG  
COMMENT OS Artificial Sequence  
PN JP 2002526116-A/33  
PD 20-AUG-2002  
PF 05-OCT-1999 JP 2000574707  
PR 07-OCT-1998 US 09/167362, 07-OCT-1998 US 09/168231 PI  
PETER BERNARD HEIFETZ, STEPHEN ARTHUR GOFF, ANNMARIE BLOOM PI TUTTLE.  
PC MONIKA ELSE GRIOT WENK  
PC A01H5/00, A23L1/30, A23L1/30, A61K38/00, A61K38/16, A61K38/22, PC A61K38/28,  
PC A61K38/43, A61K39/00, A61K39/35, A61P29/00, A61P37/00, A61P37/06, PC A61P37/08,

PC C12N5/10,C12N15/09/(C12N5/10,C12R1:91),C12N15/00,C12N5/00, PC  
A61K37/02,  
PC A61K37/26,A61K37/48,A61K37/04,A61K37/24,(C12N5/00,C12R1:91) CC  
Description of Artificial Sequence: oligonucleotide FH Key  
Location/Qualifiers  
FT source 1..28  
FT /organism='Artificial Sequence'.  
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ORIGIN  
Query Match 67.8%; Score 12.2; DB 6; Length 28;  
Best Local Similarity 82.4%; Pred.No. 2.6e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TGCCTTGAGAACTTCGG 17  
| | | | | | | | | | | | | | | | | | | |  
Db 26 TTCTCGGAGATCTTCGG 10  
Search completed: March 3, 2006, 08:38:52  
Job time : 378.932 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:02:58 ; Search time 117.534 Seconds  
(without alignments)  
1020.680 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18  
Sequence: 1 tgccttgagaacttcggg 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 496997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : N Geneseq\_21.1\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	100.0	18	AAH47977	Aah47977 Human ind
2	14.8	82.2	24	ADW47303	Adw47303 Osteopor
3	14	77.8	29	ADW47302	Adw47302 Osteopor
4	13.8	76.7	20	ABK30534	Abk30534 Human gli
5	13.8	76.7	25	ACI93355	Acti93355 Human mic
6	13.4	74.4	30	AAT10512	Aat10512 5' primer
7	13.4	74.4	30	ADO79688	Ado79688 DPF3 PCR
8	13.4	74.4	30	ADY02087	Ady02087 PCR prime
9	13.2	73.3	20	ADT75569	Adt75569 S. pneumo
10	13.2	73.3	29	AAQ70160	Aaq70160 Primer fo
11	13.2	73.3	51	AAA77010	Aaa77010 Human clo
12	13.2	73.3	51	AAA77011	Aaa77011 Human clo
13	13.2	73.3	51	AAL27669	Aal27669 Human SNP
14	13.2	73.3	60	ADQ07709	Adq07709 PCR prime
15	13.2	73.3	65	ABN52445	Abn52445 Mouse spl
16	13	72.2	21	AAQ79424	Aaq79424 PCR prime
17	13	72.2	50	ADD41511	Add41511 Synthetic
18	13	72.2	63	ADM68520	Adm68520 BtSim rel
19	13	72.2	65	ABN51708	Abn51708 Mouse spl

ADP18282	HEX1 gene
ABQ03710	Oligonucle
ADY26567	PCR prime
ABK88169	Human nuc
ABX15037	Human bet
ADW12549	Human bet
ADP15613	Renal cel
ADR72557	Hypoxia-r
ABK05923	Human NOG
ABK20971	Human ERG
AAG91615	Human apo
ABN44183	Human spl
ABN35404	Human spl
ABN38954	Human spl
ABX92845	C2 domain
ADP21643	PCR prime
AAX23815	Bacillus
AAA07919	Secretabl
ABT11169	Human S-1
ADO40181	Human MAP
ADO40147	Human MAP
ADJ18135	Human Na+
ADA37146	Human gli
ACI11241	Human mic
ACI93354	Human mic
ACI07700	Human mic
ADC06685	PCR prime
AAA29801	Ragweed p
AAD21607	Ragweed m
ADR49359	C. elegans
ADY99464	PCR prime
AAT66460	BR110 ant
AAA38045	PCR prime
ADZ71340	Novel cys
ABZ02198	Human leu
AHH89363	Human kin
AHH38192	Human SNP
ABN58733	Human spl
ABN38892	Human spl
ABN44896	Human spl
ABN40956	Human spl
ABN55391	Mouse spl
ABN53741	Mouse spl
ADM95797	Rat antis
ADI83174	HCV DNAB
ABY91933	Coryneb
ACI67569	Human mic
ADB99175	Human PSM
ADJ93247	Human pro
ADN97349	Human C-m
AAL29615	Human SNP
AEB46491	Probe for
ADU10451	Solid tum
AAAL8811	Human TIE
AAAL8812	Human TIE
ADX82734	Medterra
ADX83030	Medterra
AAT38948	HIV-1 HXB
AAL71914	PCR prime
ADN48459	Haemoglob
ADX83031	Medterra
ADX82735	Medterra
ACF58382	Beta-glob
ADX83032	Medterra
AAX93408	PCR prime
AAG61768	Lentiviru
ABQ74654	STEAP gen
ABX12662	Non-cycli
ADC52099	Caenorhab
ADI27596	Human DRA
ADI27524	Human DRA
ADH80300	STEAP PCR

C 93 11.8 65.6 20 12 ADK80872 Chimeric  
 C 94 11.8 65.6 20 12 ADK77211 Chimeric  
 C 95 11.8 65.6 20 12 ADK81043 Chimeric  
 C 96 11.8 65.6 20 12 ADK76762 Chimeric  
 C 97 11.8 65.6 20 12 ADK76861 Chimeric  
 C 98 11.8 65.6 20 12 ADK78504 Chimeric  
 C 99 11.8 65.6 20 13 ADQ99869 Rice SNP  
 C 100 11.8 65.6 20 13 ADR57958 ICER gene

## ALIGNMENTS

RESULT 1  
 AAH47977  
 ID AAH47977 standard; DNA; 18 BP.  
 XX AC  
 XX AAH47977;  
 XX AC  
 XX 02-OCT-2001 (first entry)  
 XX DT  
 XX DE Human inducible NOS antisense oligonucleotide SEQ ID NO 21.  
 XX DE  
 XX KW Antisense oligonucleotide; inducible nitric oxide synthase; NOS;  
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;  
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
 KW 2'-O-methoxyethyl; phosphorothioate; human; ss.  
 XX KW Homo sapiens.  
 XX OS  
 XX FH Key Location/Qualifiers  
 FT modified\_base 1..18  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone, 5' and 3' four  
 FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine  
 FT residues in the 2'-MOE wings are 5-methylcytidines) and a  
 FT deoxy gap"  
 XX FT  
 XX PN WO200152902-A1.  
 XX XX  
 XX PD 26-JUL-2001.  
 XX XX  
 XX PF 15-JAN-2001; 2001WO-US001381.  
 XX XX  
 XX PR 24-JAN-2000; 2000US-00490208.  
 XX XX  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX XX  
 XX PI Bennett CF, Dean NM, Cowser LM;  
 XX XX  
 XX DR WPI; 2001-465340/50.  
 XX XX  
 XX PT New antisense oligonucleotides for modulating the expression of inducible  
 PT nitric oxide synthase in cells or tissues, particularly useful for  
 PT treating e.g. immunological, cardiovascular or neurological disorders, or  
 PT ischemia.  
 XX PT  
 XX PS Claim 3; Page 83; 144pp; English.  
 XX PS  
 XX CC The invention relates to antisense compounds, especially  
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible  
 CC nitric oxide synthase and which specifically hybridize to and modulate  
 CC expression of inducible nitric oxide synthase. The antisense compounds  
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,  
 CC neuroprotective, disorder and vasotropic activity. The antisense  
 CC oligonucleotides are useful for inhibiting the expression of inducible  
 CC nitric oxide synthase in cells or tissues. In particular, the antisense  
 CC oligonucleotides are useful for treating diseases or disorders associated  
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological  
 CC disorder, cardiovascular disease, neurological disorder or  
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also  
 CC useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a  
 CC phosphorothioate backbone, a central "gap" region of ten nucleotides  
 CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine  
 CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human  
 CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)  
 XX CC  
 SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
 |||||  
 Db 1 TGCCTTGAGAACTTCGGG 18

## RESULT 2

ADW47303/C  
 ID ADW47303 standard; DNA; 24 BP.  
 XX AC  
 XX ADW47303;  
 XX AC

DT 07-APR-2005 (first entry)

DE Osteoporosis polymorphism detection related primer, SEQ ID 9.

XX KW SNP detection; osteoporosis; tumor necrosis factor receptor; TNFR;

KW DNA detection; ss; primer; PCR.

XX OS Synthetic.

XX JP2005006538-A.

PN 13-JAN-2005.

PD 18-JUN-2003; 2003JP-00173288.

PF 18-JUN-2003; 2003JP-00173288.

XX (UYNI-) UNIV NIPPON IKA.

XX WPI; 2005-114728/13.

PT Detecting polymorphism in genes associated with osteoporosis such as  
 PT tumor necrosis factor receptor associated factor binding protein gene,  
 PT reverse-inducible LIM domain protein gene and heat shock protein 70 gene.

XX Disclosure; SEQ ID NO 9; 38pp; Japanese.

XX CC The invention relates to a novel method for detecting polymorphism in  
 CC genes associated with osteoporosis, such as a tumor necrosis factor  
 CC receptor (TNFR) associated factor binding protein gene, reverse-inducible  
 CC LIM domain protein gene, heat shock protein 70 gene, or an alpha-2-  
 CC glycoprotein 1 gene. The invention further comprises a kit for  
 CC performing gene detection, comprising components for detecting  
 CC polymorphism in genes associated with osteoporosis such as TNFR  
 CC associated factor binding protein gene, reverse-inducible LIM domain  
 CC protein gene, heat shock protein 70 gene, or an alpha-2-glycoprotein 1  
 CC gene; a kit for performing an invader assay, comprising components for  
 CC detecting polymorphisms chosen from polymorphism at base position 2141,  
 CC 1542 or 525 of TNFR associated factor binding protein gene, polymorphism  
 CC at base position 6364 in sequence of reverse-inducible LIM domain protein  
 CC gene, polymorphism at a base that encodes glutamic acid of position 110  
 CC in amino acid sequence of heat shock protein 70 gene, and polymorphism at  
 CC base position 1115 in base sequence of alpha-2-glycoprotein 1 gene; and a  
 CC kit for performing gene detection by the invader assay. The method is  
 CC useful for detecting a polymorphism in genes associated with  
 CC osteoporosis, preferably postmenopausal osteoporosis. The method is also  
 CC useful in an invader assay for detecting a gene. This polynucleotide  
 CC sequence represents a primer used in the exemplification of the  
 CC invention.



SQ Sequence 24 BP; 8 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 82.2%; Score 14.8; DB 14; Length 24;  
Best Local Similarity 88.9%; Pred. No. 5.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGG 18  
DB 18 TGCCTTGAGAACTTAAG 1

RESULT 3  
ADW47302/c  
ID ADW47302 standard; DNA; 29 BP.  
XX  
AC ADW47302;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Osteoporosis polymorphism detection related primer, SEQ ID 8.  
XX  
KW SNP detection; osteoporosis; tumor necrosis factor receptor; TNFR;  
KW DNA detection; ss; primer; PCR.  
XX  
OS Synthetic.  
XX  
PN JP2005006538-A.  
XX  
PD 13-JAN-2005.  
XX  
PF 18-JUN-2003; 2003JP-00173288.  
XX  
PR 18-JUN-2003; 2003JP-00173288.  
XX  
PA (UYN1-) UNIV NIPPON IKA.  
XX  
DR WPI; 2005-114728/13.  
XX  
PT Detecting polymorphism in genes associated with osteoporosis such as  
PT tumor necrosis factor receptor associated factor binding protein gene,  
PT reverse-inducible LIM domain protein gene and heat shock protein 70 gene.  
XX  
PS Disclosure; SEQ ID NO 8; 38pp; Japanese.  
XX  
CC The invention relates to a novel method for detecting polymorphism in  
CC genes associated with osteoporosis, such as a tumor necrosis factor  
CC receptor (TNFR) associated factor binding protein gene, reverse-inducible  
CC LIM domain protein gene, heat shock protein 70 gene, or an alpha-2-  
CC glycoprotein 1 gene. The invention further comprises: a kit for  
CC performing gene detection, comprising components for detecting  
CC polymorphism in genes associated with osteoporosis such as TNFR  
CC associated factor binding protein gene, reverse-inducible LIM domain  
CC protein gene, heat shock protein 70 gene, or an alpha-2-glycoprotein 1  
CC gene; a kit for performing an invader assay, comprising components for  
CC detecting polymorphisms chosen from polymorphism at base position 2141,  
CC 1542 or 525 of TNFR associated factor binding protein gene, polymorphism  
CC at base position 5364 in sequence of reverse-inducible LIM domain protein  
CC gene, polymorphism at a base that encodes glutamic acid of position 110  
CC in amino acid sequence of heat shock protein 70 gene, and polymorphism at  
CC base position 1115 in base sequence of alpha-2-glycoprotein 1 gene; and a  
CC kit for performing gene detection by the invader assay. The method is  
CC useful for detecting a polymorphism in genes associated with  
CC osteoporosis, preferably postmenopausal osteoporosis. The method is also  
CC useful in an invader assay for detecting a gene. This polynucleotide  
CC sequence represents a primer used in the exemplification of the  
XX invention.

SQ Sequence 29 BP; 8 A; 3 C; 8 G; 10 T; 0 U; 0 Other;  
Query Match 77.8%; Score 14; DB 14; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGG 18  
DB 18 TGCCTTGAGAACTTAAG 1

RESULT 4  
ABK30534/c  
ID ABK30534 standard; DNA; 20 BP.  
XX  
AC ABK30534;  
XX  
DT 23-APR-2002. (first entry)  
XX  
DE Human glioma-associated oncogene-1 antisense oligonucleotide ISIS 124866.  
XX  
KW Human; glioma-associated oncogene-1 associated disease; infection;  
KW inflammation; tumour formation; cytostatic; antiinflammatory; antisense;  
KW phosphorothioate; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6329203-B1.  
XX  
PD 11-DEC-2001.  
XX  
PF 08-SEP-2000; 2000US-00657042.  
XX  
PR 08-SEP-2000; 2000US-00657042.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Wyatt J;  
XX  
DR WPI; 2002-138363/18.  
XX  
PT Novel antisense compounds targeted to nucleic acids encoding glioma-  
PT associated oncogene-1, for modulating the gene expression and treating  
PT diseases associated with expression of the oncogene in humans.  
XX  
PS Example 15; Col 45-46; 43pp; English.  
XX  
CC The present invention relates to antisense compounds and methods for  
CC modulating the expression of human glioma-associated oncogene-1. The  
CC antisense compounds, particularly antisense oligonucleotides, target and  
CC inhibit the expression of human glioma-associated oncogene-1. The  
CC antisense compounds are useful for inhibiting the expression of human  
CC glioma-associated oncogene-1 in human cells or tissues and for treating  
CC an animal, particularly a human suspected of having or being prone to a  
CC disease or condition associated with expression of glioma-associated  
CC oncogene-1. The compounds are useful for diagnostics, therapeutics and as  
CC research reagent, e.g. prophylactically to prevent or delay infection,  
CC inflammation or tumour formation. The antisense compounds are safely and  
CC effectively administered to humans. ABK30509-ABK30586 represent the  
CC antisense oligonucleotides of the invention which comprise a  
XX phosphorothioate backbone

SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 76.7%; Score 13.8; DB 6; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18  
DB 18 GCCTTGAGAACTTCAG 2

RESULT 5  
ACI93355/c  
ID ACI93355 standard; DNA; 25 BP.  
XX  
AC ACI93355;  
XX

DT 14-OCT-2003 (first entry)  
 XX Human microarray DNA oligonucleotide SEQ ID NO 93346.  
 DE EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 XX genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX Homo sapiens.  
 XX US2003104410-A1.  
 PN 05-JUN-2003.  
 XX 15-MAR-2002; 2002US-00098263.  
 PF 16-MAR-2001; 2001US-0276759P.  
 XX (AFFY-) AFFYMETRIX INC.  
 PA Mittmann MP;  
 PI WPI; 2003-567953/53.  
 XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX Claim 1; SEQ ID NO 93346; 9pp; English.  
 PS The invention discloses a microarray comprising a plurality of nucleic  
 XX acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 76.7%; Score 13.8; DB 9; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TGCCCTTGAGAACTTCGG 17  
 ||||| ||||| ||||| ||||| |||||  
 Db 23 TGCCTTAAGAACGTCGG 7  
 RESULT 6  
 AAT10512  
 ID AAT10512 standard; DNA; 30 BP.  
 XX AAT10512;  
 AC 12-JUL-1996 (first entry)  
 XX 12-JUL-1996 (first entry)  
 DT 12-JUL-1996 (first entry)  
 XX

DE 5' primer for rabbit beta-globin intron amplification.  
 XX transgenic mouse; thyroid hormone receptor; retinoic acid receptor;  
 KW screen; antagonist; agonist; signal transduction mechanism; variant;  
 KW primer; antisense; PCR; polymerase chain reaction; ss.  
 XX Synthetic.  
 XX JP07327548-A.  
 PN 19-DEC-1995.  
 XX 13-JUN-1994; 94JP-00154201.  
 PF 13-JUN-1994; 94JP-00154201.  
 PR (ONOH ) ONO PHARM CO LTD.  
 XX WPI; 1996-072216/08.  
 DR Transgenic mouse contg. mutant human retinoic acid receptor alpha gene -  
 XX used to screen for agonists or antagonists of human retinoic acid  
 PT receptor, and elucidate the receptor's signal transduction mechanism.  
 PT Example 2; Page 4; 7pp; Japanese.  
 PS AAT10512-13 are used to PCR amplify a 0.7 kb rabbit beta-globin intron  
 XX sequence, used in the construction of expression vector pG32-K14. The  
 CC expression vector contains the keratin-14 promoter used to control a  
 CC heterogenous gene, e.g. human retinoic acid receptor variant gene. The  
 CC invention concerns generating transgenic mice contg. a gene (introduced  
 CC under the control of the keratin-14 promoter) encoding a mutant human  
 CC retinoic acid receptor alpha. These mice can be used to screen for  
 CC (ant)agonists or to elucidate the signal transduction mechanism  
 XX Sequence 30 BP; 7 A; 4 C; 9 G; 10 T; 0 U; 0 Other;  
 SQ Query Match 74.4%; Score 13.4; DB 2; Length 30;  
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 CTTGAGAACTTCGG 18  
 ||||| ||||| ||||| ||||| |||||  
 Db 8 CTTGAGAACTTCAGG 22  
 RESULT 7  
 ADO79688  
 ID ADO79688 standard; DNA; 30 BP.  
 XX ADO79688;  
 AC 26-AUG-2004 (first entry)  
 XX DP3 PCR primer #22.  
 DE Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DP3;  
 KW CENPC1; SNP; single nucleotide polymorphism;  
 KW D4; zinc and double PHD fingers, family 3; CERD4; cer-d4; FLJ14079;  
 KW 2810403B03Rik; Rho family guanine-nucleotide exchange factor;  
 KW chromosome 14q24.3-q31.1; PCR; primer; ss.  
 XX Homo sapiens.  
 OS WO2004047514-A2.  
 XX 10-JUN-2004.  
 PD 25-NOV-2003; 2003WO-US037943.  
 XX 25-NOV-2002; 2002US-0429136P.  
 PR 24-JUL-2003; 2003US-0490234P.  
 XX

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PA (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
XX WPI; 2004-441037/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of polymorphic variations in the DLG1, KIAA0783, DPf3 or CENPC1 regions
XX which are associated with breast cancer in a nucleic acid sample from a
XX subject.
XX
XX Example 5; Page 82; 227pp; English.
XX
XX The present invention relates to a method for identifying a subject at
XX risk of breast cancer. The method comprising detecting the presence or
XX absence of one or more polymorphic variations associated with breast
XX cancer in a nucleic acid sample from a subject. The nucleic acid sample
XX comprises the DLG1 region (AD079402), KIAA0783 region (AD079403), DPf3
XX region (AD079404) or CENPC1 region (AD079405). The gene DLG1 (discs,
XX large homolog 1 (Drosophila)) is also known as synapse-associated protein
XX 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
XX gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
XX has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
XX novel gene with unknown function, however, being a zinc finger protein,
XX it likely to be a transcription factor. The gene DPf3 (D4, zinc and
XX double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079
XX and 2810403803Rik. DPf3 is a Rho family guanine-nucleotide exchange
XX factor. DPf3 has been mapped to chromosomal position 14q24.3-q31.1. The
XX gene CENPC1 (centromere protein C1) is also known as Centromere
XX autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-
XX q13.3. CENPC1 is a centromere autoantigen and a component of the inner
XX kinetochore plate. The CENPC1 protein is required for maintaining proper
XX kinetochore size and a timely transition to anaphase. The method is
XX useful for identifying a subject at risk of breast cancer, for early
XX diagnosis, prevention and treatment of breast cancer, to analyze and
XX predict a response to a breast cancer treatment, and in clinical drug
XX trials. The present sequence was used in an example from the invention.
XX
XX Sequence 30 BP; 6 A; 8 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 12; Length 30;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TGCCCTTGAGAACTTC 15
XX ||||| |||||
XX Db 9 TGCCCTTGAGAACTTC 23
XX
XX RESULT 8
XX ADY02087
XX ID ADY02087 standard; DNA; 30 BP.
XX
XX AC ADY02087;
XX
XX XX 05-MAY-2005 (first entry)
XX
XX DE PCR primer 791 used to amplify human DPf3 SNP DNA.
XX
XX XX SNP detection; breast tumor; endocrine disease;
XX KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
XX KW gene therapy; RNA interference; ss; PCR; primer;
XX KW D4, zinc and double PHD fingers, family 3; DPf3;
XX KW guanine-nucleotide exchange factor.
XX
XX OS Homo sapiens.
XX
XX XX WO2005014846-A2.
XX
XX PD 17-FEB-2005.
XX
XX XX 27-MAY-2004; 2004WO-US016939.
XX
XX

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PR 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX Hoyal-Wrightson CR;
XX
XX WPI; 2005-163257/17.
XX
XX Identifying risk of, preventing and/or treating breast cancer by
XX identifying and/or analyzing polymorphic variations in nucleotide
XX sequences within the human genome.
XX
XX Example 16; Page 245; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer comprising detecting the presence or absence of a
XX polymorphic variation associated with breast cancer. The method of the
XX invention demonstrates cytostatic activity and may be useful for
XX identifying a risk of, preventing and/or treating breast cancer and
XX cancer metastasis. The methods may be utilized for gene therapy or RNA
XX interference. The current sequence is that of a PCR primer of the
XX invention which was used to amplify a human rho-family guanine-nucleotide
XX exchange factor D4, zinc and double PHD fingers, family 3 (DPF3) DNA
XX containing a single nucleotide polymorphism (SNP).
XX
XX Sequence 30 BP; 6 A; 8 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 14; Length 30;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TGCCCTTGAGAACTTC 15
XX ||||| |||||
XX Db 9 TGCCCTTGAGAACTTC 23
XX
XX RESULT 9
XX ADT75569/c
XX ID ADT75569 standard; DNA; 20 BP.
XX
XX AC ADT75569;
XX
XX DT 13-JAN-2005 (first entry)
XX
XX DE S. pneumoniae PCR primer SEQ ID NO 277.
XX
XX KW Streptococcus pneumoniae; cpsA; cpsB; wzy; wzx; microarray; serotype; ss;
XX KW PCR; primer.
XX
XX OS Streptococcus pneumoniae.
XX
XX XX WO2004090159-A1.
XX
XX PD 21-OCT-2004.
XX
XX PF 13-APR-2004; 2004WO-AU0000480.
XX
XX PR 10-APR-2003; 2003AU-00901717.
XX
XX PA (WSYD-) WESTERN SYDNEY AREA HEALTH SERVICE.
XX PA (TIAN-) TIANJIN BIOCHIP TECHNOLOGY CORP.
XX
XX Kong F, Gilbert G, Wang L, Liu D, Tao J;
XX WPI; 2004-748779/73.
XX
XX Determining Streptococcus pneumoniae serotypes, useful in monitoring the
XX epidemiology of invasive S. pneumoniae infections, comprises analyzing
XX cpsA and cpsB gene and/or wzy and/or wzx gene.
XX

```



Qy 1 TGCCTTGAGAACTTCGG 18  
||| | ||| | ||| |  
Db 33 TGCTTAGAGACCTTCGG 50

RESULT 12

AAA77011  
ID AAA77011 standard; cDNA; 51 bp.

AAA77011:

16-NOV-2000 (first entry)

Human clone cc43054295 polymorphic site. SEQ ID NO: 694.

AA Human; single nucleotide polymorphism; SNP; chromosome X; detection;  
 KW identification; gene therapy; ss.

OS Homo sapiens.

xx	Key	Location/Qualifiers
FH		replace(26,C)
FT	variation	/*tag= a
FT		

PN WO200029623-A2.

25-MAY-2000.

17-NOV-1999: 99WO-US027293

PR 17-NOV-1998: 98US-0109024P.

PR 16-NOV-1999; 99US-00443199;

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach MD;

WPI: 2000-387826/33.

PT Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.

PS Claim 1: Page 367: 543pp: English.

Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result in non-conservative changes. The SNPs in sequences 1187 to 1192 (AAA77504-A77509) generate frameshift mutations. The invention also relates to a method of detecting a polymorphic site in a nucleic acid and a method of determining the relatedness of two nucleic acids. It also encompasses peptides containing polymorphic sites, antibodies raised against such peptides, and a method of detecting polymorphic proteins/peptides using the antibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence polymorphism. Such treatment would comprise administration of the wild-type nucleic acid sequence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals

Sequence 51 BP: 8 A: 11 C: 23 G: 9 T: 0 U: 0 Other:

Query Match 73.3%; Score 13.2; DB 3; Length 51;  
Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels

Qy 1 TGCCTTGAGAACTTCGGG 18  
Db 33 TGCTTAGAGACCTTCGGG 50

RESULT 13

AAL27669  
 ID AAL27669 standard; DNA; 51 BP.

AC AAL27669:

24-JAN-2002 (first entry)

Human SNP oligonucleotide #877.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease. ss.

OS Homo sapiens.

PN WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US035498.

PR 28-DEC-1999: 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA. Leach M:

WPI: 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

PS Claim 1: Page 1633: 4143pp: English.

CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms

Sequence 51 BP; 12 A; 19 C; 14 G; 6 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 51;  
Best Local Similarity 83.3%; Pred. No. 4.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels

Qy 1 TGCCTTGAGAACTTCGGG 18  
db 25 TGCCTCCAGAACTTCGGG 42

PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-1B001903.  
XX  
PR 28-JUL-2000; 2000US-0221607P.  
PR 02-MAY-2001; 2001US-0287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
PI WPI; 2002-257383/30.  
XX  
DR  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
XX Example 1; SEQ ID NO 25193; 47pp; English.  
XX  
CC The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 65 BP; 10 A; 19 C; 18 G; 18 T; 0 U; 0 Other;  
Query Match 73.3%; Score 13.2; DB 6; Length 65;  
Best Local Similarity 83.3%; Pred. No. 4.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TGCCTTGAGAACTTCGGG 18  
||||| |||||  
Db 3 TGCCTTCAGTACTTCGTG 20  
RESULT 16  
AAQ79424/c  
ID AAQ79424 standard; DNA; 21 BP.  
XX  
AC AAQ79424;  
XX  
DT 25-MAR-2003 (revised)  
DT 03-JUN-1995 (first entry)  
XX  
DE PCR primer no. 12 based on human hepatocyte inducible nitric oxide  
DE synthase (iNOS) cDNA.  
XX  
KW Nitric oxide synthase; diabetes mellitus; PCR primer; ss.  
XX  
OS Synthetic.  
XX

PN WO2004053123-A1.  
XX  
PD 24-JUN-2004.  
XX  
PF 04-DEC-2003; 2003WO-JP015571.  
XX  
PR 10-DEC-2002; 2002JP-00357566.  
XX  
PA (KAZU-) KAZUSA DNA RES INST FOUND.  
XX  
PI Nagase T, Nakajima D, Ohara O;  
XX  
XX WPI; 2004-480936/45.  
XX  
XX New template vector for trap vectors comprises a replication origin, a  
PT drug tolerance gene, first and second primer binding sequences, and a  
PT suicide gene interposed between the primer binding sequences.  
XX  
XX Example 2; Page 16; 34pp; Japanese.  
XX  
CC The specification describes a template vector for trap vectors containing  
CC a replication origin, a drug tolerance gene, a primer binding sequence, a  
CC second primer binding sequence and a suicide gene interposed between the  
CC first and second primer binding sequences. The cloning vector is useful  
CC as an entry clone in Gateway (RTM) technology. The target open reading  
CC frame (ORF) can be accurately, quickly and conveniently cloned by  
CC homologous recombination. The present sequence represents a PCR primer  
CC which is used to amplify a talin ORF. The amplified fragment is used in  
CC the course of the invention.  
XX  
XX SQ Sequence 60 BP; 15 A; 16 C; 13 G; 15 T; 0 U; 1 Other;  
Query Match 73.3%; Score 13.2; DB 12; Length 60;  
Best Local Similarity 83.3%; Pred. No. 4.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TGCCTTGAGAACTTCGGG 18  
||||| |||||  
Db 17 TGCCTTCAGAGCTTCGAG 34  
RESULT 15  
ABN52445  
ID ABN52445 standard; DNA; 65 BP.  
XX  
AC ABN52445;  
XX  
DT 15-JUL-2002 (first entry)  
DT  
XX  
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25193.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Mus musculus.  
XX

PN WO9424269-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 11-APR-1994; 94WO-DK000146.  
XX  
PR 16-APR-1993; 93DK-00000433.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
PI Karlsen AE;  
XX  
DR WPI; 1994-341851/42.  
XX  
PT New DNA encoding inducible pancreatic islet nitric oxide synthase - and  
PT related vectors and transformed cells, useful for identifying specific  
PT inhibitors for treatment or prevention of insulin dependent diabetes  
PT mellitus.  
XX  
PS Example; Page 25; 36pp; English.  
XX  
CC Human islets were incubated in a mixture of IL-1, TNF-alpha and IFN-  
CC gamma. The human islet iNOS was cloned by RT-PCR on the isolated mRNA  
CC with primers based on the human hepatocyte sequence. The sequence of the  
CC primers is given in AAQ79424 and AAQ79425. The clone human islet iNOS was  
CC sequenced. The 5' UTR and translated human islet iNOS is given in  
CC AAQ79426, and the 3' end in AAQ79427. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 72.2%; Score 13; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TGCCTTGAGAACT 13  
DB 13 TGCCTTGAGAACT 1  
  
RESULT 17  
ADD41511/c  
ID ADD41511 standard; DNA; 50 BP.  
XX  
AC ADD41511;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Synthetic insecticidal toxin gene (cryIAC) production PCR primer #54.  
XX  
KW synthetic insecticidal toxin gene; cryIAC; diamondback moth; PCR; primer;  
KW ss.  
XX  
OS Synthetic.  
OS Unidentified.  
XX  
PN KR2002013003-A.  
XX  
PD 20-FEB-2002.  
XX  
PF 10-AUG-2000; 2000KR-00046327.  
XX  
PR 10-AUG-2000; 2000KR-00046327.  
XX  
PA (RURA-) RURAL DEV ADMINISTRATION.  
XX  
PI Cho HS, Jin YM, Kim HI, Park BS;  
XX  
DR WPI; 2002-747866/81.  
XX  
PT Synthetic insecticidal toxin gene for transformation of brassica plants.  
XX  
PS Example 2; Page 15; 23pp; Korean.  
  
XX The invention comprises a synthetic insecticidal toxin gene (cryIAC) for  
CC the transformation of Brassicae plants. The cryIAC gene is useful for  
CC preventing plants from being damaged by the diamondback moth (Plutella  
CC xylostella). The present DNA sequence represents a PCR primer that was  
CC used in the construction of the cryIAC gene of the invention.  
XX  
SQ Sequence 50 BP; 16 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
  
Query Match 72.2%; Score 13; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CTTGAGAACTTCG 16  
DB 33 CTTGAGAACTTCG 21  
  
RESULT 18  
ADM68520  
ID ADM68520 standard; DNA; 63 BP.  
XX  
AC ADM68520;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE BtS1m related oligonucleotide #17.  
XX  
KW Insecticidal protein; BtS1m; ss.  
XX  
OS Synthetic.  
XX  
PN CN1393561-A.  
XX  
PD 29-JAN-2003.  
XX  
PF 22-JUN-2001; 2001CN-00129519.  
XX  
PR 22-JUN-2001; 2001CN-00129519.  
XX  
PA (MICR-) INST MICROBES CHINESE ACAD SCI.  
XX  
PI Tian Y, Qin H, Guo H;  
XX  
DR WPI; 2003-469217/45.  
XX  
PT Mosaic insecticidal protein gene able to secrete its product to outside  
PT of cell.  
XX  
PS Example 1; Page 14; 46pp; Chinese.  
XX  
CC The present invention relates to an artificially synthetic mosaic  
CC insecticidal protein gene Bt1m of Bacillus thuringiensis (Bt) which can  
CC be effectively expressed in higher plant. By adding a secretory signal  
CC peptide coding sequence to the terminal 5' of the said gene can generate  
CC a fusion protein gene Bt-S1m (ADM68502). The insecticidal protein Bt  
CC (ADM68503) expressed by the gene in plant can be secreted in the gap  
CC between cells, so improving the stability of insecticidal protein and  
CC reducing the interference of insecticidal protein to normal cell  
CC function. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 63 BP; 14 A; 17 C; 16 G; 16 T; 0 U; 0 Other;  
  
Query Match 72.2%; Score 13; DB 11; Length 63;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CTTGAGAACTTCG 16  
DB 13 CTTGAGAACTTCG 25  
  
RESULT 19

```
ABN51708
ID ABN51708 standard; DNA; 65 BP.
XX
AC ABN51708;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:24456.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 24456; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX )transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The
XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a particular
XX biological or pathological state, and so allowing the detection of tissue
XX - and pathology-specific genes such as those genes only expressed in
XX specific tissue under a specific pathological condition; to detect
XX developmental specific genes; and to detect RNA transcripts and splice
XX variants of a transcriptome of a patient suffering from a particular
XX disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX rats, humans and mice, which are used in the exemplification of the
XX present invention. N.B. The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 13 A; 20 C; 17 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 72.2%; Score 13; DB 6; Length 65;
XX Best Local Similarity 100.0%; Pred. No. 6.1e+03;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 TGAGAACTTCGGG 18
DB 10 TGAGAACTTCGGG 22
XX
XX RESULT 20
ADP18282
```

```
ADP18282 standard; DNA; 20 BP.
XX
AC ADP18282;
XX
DT 29-JUL-2004 (first entry)
XX
DE HEX1 gene antisense primer seqid 24.
XX
KW cytostatic; senescence; cell proliferation; neoplastic cell growth;
KW cellular gene expression; reverse transcriptase PCR; RT-PCR; primer; ss;
KW doxorubicin-induced senescence; HCT 116 cell; human.
XX
OS Homo sapiens.
XX
PN US2004058320-A1.
XX
PD 25-MAR-2004.
XX
PF 21-DEC-2001; 2001US-00032264.
XX
PR 21-DEC-2000; 2000US-0257907P.
PR 17-DEC-2001; 2001US-0341425P.
XX
PA (RONI/) RONINSON I B.
PA (CHAN/) CHANG B.
XX
PI Roninson IB, Chang B;
XX
DR WPI; 2004-294237/27.
XX
XX Identifying a compound that induces senescence in a mammalian cell,
XX useful for treating abnormal cell proliferation, comprises assaying
XX expression of a cellular gene in the cell in the presence and in the
XX absence of a compound.
XX
PS Example 2; SEQ ID NO 24; 29pp; English.
XX
XX The invention describes a method of identifying a compound that induces
XX senescence in a mammalian cell. The method comprises: culturing the
XX mammalian cell in the presence and absence of the compound; assaying the
XX expression of at least one cellular gene selected from 73 genes given in
XX the specification, in the cell in the presence and in the absence of the
XX compound; and identifying compounds that induce senescence when
XX expression of at least one of the cellular gene is higher in the presence
XX of the compound than in the absence of the compound. Also described are:
XX a compound that induces senescence in a mammalian cell identified from
XX the method above; assessing efficacy of a treatment of a disease or
XX condition relating to abnormal cell proliferation or neoplastic cell
XX growth; and identifying a compound that inhibits senescence-associated
XX induction of cellular gene expression. Compounds that induce senescence
XX in abnormally proliferating or neoplastic cells are useful for treating a
XX disease or condition relating to abnormal cell proliferation or
XX neoplastic cell growth. This sequence represents a reverse transcriptase
XX PCR primer used to identify genes induced and repressed following
XX doxorubicin-induced senescence of HCT 116 cells.
XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 71.1%; Score 12.8; DB 12; Length 20;
XX Best Local Similarity 87.5%; Pred. No. 6.7e+03;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GCCTTCAGAACTTCGG 17
DB 2 GCCTTCAGAACTTCAG 17
XX
XX RESULT 21
ABQ03710/c
ID ABQ03710 standard; DNA; 24 BP.
XX
AC ABQ03710;
XX
```



DT 11-JUN-2002 (first entry)  
XX Oligonucleotide adapter/capture probe 3701.  
XX  
KW Oligonucleotide array; adapter sequence; probe; ss.  
OS Synthetic.  
XX WO200216649-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 27-AUG-2001; 2001WO-US026519.  
XX  
XX 25-AUG-2000; 2000US-0227948P.  
XX 29-AUG-2000; 2000US-0228854P.  
XX (ILLU-) ILLUMINA INC.  
XX Gunderson K;  
XX  
XX WPI; 2002-292068/33.  
XX  
XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
XX Claim 1; Page 132; 261pp; English.  
XX  
XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ0010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
XX Sequence 24 BP; 6 A; 8 C; 7 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 71.1%; Score 12.8; DB 6; Length 24;  
Best Local Similarity 87.5%; Pred. No. 6.9e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TGCCTTGAGACTTCG 16  
Db 23 TGCCTTGAGACTTCG 8

RESULT 22  
ADY26567/c  
ID ADY26567 standard; DNA; 36 BP.  
XX  
XX AC ADY26567;  
XX  
XX 05-MAY-2005 (first entry)  
XX  
XX PCR primer #1 used to amplify DNA encoding a human dicer mutant.  
XX  
XX dsRNA degradation; dicer; RNaseIIIa; RNaseIIIb; PAZ domain; PCR; primer;  
KW ss.  
XX Homo sapiens.  
XX Synthetic.  
XX WO2005017144-A1.  
XX  
XX 24-FEB-2005.  
XX  
XX 10-AUG-2004; 2004WO-JP011480.  
XX  
XX 14-AUG-2003; 2003JP-00293553.  
PR

PR 30-SEP-2003; 2003JP-00342126.  
PR 08-DEC-2003; 2003JP-00409639.  
PR 24-MAR-2004; 2004JP-00086129.  
XX  
XX (TAKI ) TAKARA BIO INC.  
XX  
XX Sagawa H, Tomono J, Ueno H, Kato I;  
XX WPI; 2005-182369/19.  
XX  
XX Methods for degrading dRNAs and synthesizing RNAs of definite length,  
PT comprises employing specific enzymatic proteins, used e.g. in RNA  
PT interference and other applications in medical and biological fields.  
XX  
XX Example 1; SEQ ID NO 5; 56pp; Japanese.  
XX  
XX The specification describes a protein with a dsRNA degrading activity,  
CC that is capable of acting on a dsRNA to form a dsRNA of a definite  
CC length. The protein has a functional domain of dicer which is composed of  
CC RNaseIIIa and b as well as a dsRNA-binding domain, particularly a PAZ  
CC domain too. The protein of the invention is useful for degrading dRNAs  
CC and synthesizing RNAs of definite length which are useful, e.g. for RNA  
CC interference and in other applications in medical and biological fields  
CC particularly and genetic engineering. PCR primers ADY26567-ADY26568 were  
CC used to amplify DNA encoding a human dicer protein mutant.  
XX  
XX Sequence 36 BP; 8 A; 10 C; 12 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 71.1%; Score 12.8; DB 14; Length 36;  
Best Local Similarity 87.5%; Pred. No. 7.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 CCTTGAGACTTCGGG 18  
Db 28 CCTTGAGACTTCGGG 13

RESULT 23  
ABK88169/c  
ID ABK88169 standard; DNA; 41 BP.  
XX  
XX AC ABK88169;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Human nucleotide excision repair protein 13.75, probe #1.  
XX  
XX Human; nucleotide excision repair protein 13.75;  
KW embryo development distortion; tumour; Cockayne syndrome; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX CN1340517-A.  
XX  
XX 20-MAR-2002.  
XX  
XX 31-AUG-2000; 2000CN-00119815.  
XX  
XX 31-AUG-2000; 2000CN-00119815.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-436411/47.  
XX  
XX Polypeptide-human nucleotide excision repair protein 13.75 and  
PT polynucleotide for coding it.  
XX  
XX Example 6; Page 21 (Disclosure); 35pp; Chinese.  
XX  
XX The invention describes a novel polypeptide-human nucleotide excision  
CC repair protein 13.75, the polynucleotide encoding it and the process for



Search completed: March 3, 2006, 08:00:33  
Job time : 123.534 secs

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*This Page Blank (usp10)*

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds  
(without alignments)  
1353.240 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18

Sequence: 1 tgccttgagaacttcggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:  
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4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/prodata/1/ina/H\_COMB.seq:  
6: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:  
7: /cgn2\_6/prodata/1/ina/PP\_COMB.seq:  
8: /cgn2\_6/prodata/1/ina/RE\_COMB.seq:  
9: /cgn2\_6/prodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	13.2	73.3	21	3	US-10-131-827-8979
C 3	13.2	73.3	25	3	US-09-396-196G-1069
C 4	13.2	73.3	25	3	US-09-396-196G-54888
C 5	13.2	73.3	25	3	US-09-396-196G-68119
C 6	13.2	73.3	51	3	US-09-443-199C-693
C 7	13.2	73.3	51	3	US-09-443-199C-694
C 8	12.4	68.9	25	3	US-09-998-547-5
C 9	12.4	68.9	25	3	US-09-396-196G-54889
C 10	12.4	68.9	25	3	US-09-396-196G-75625
C 11	12.4	68.9	25	3	US-09-396-196G-75626
C 12	12.4	68.9	32	3	US-08-991-525B-86
C 13	12.4	68.9	39	2	US-08-456-840-11
C 14	12.4	68.9	39	2	US-08-266-407A-11
C 15	12.4	68.9	39	2	US-08-892-544-11
C 16	12.4	68.9	68	2	US-07-982-712-14
C 17	12.4	68.9	80	3	US-09-149-727-59
C 18	12.4	68.9	80	3	US-09-270-957-98
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C 20	12.2	67.8	25	3	US-09-396-196G-26393
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C 22	12.2	67.8	25	3	US-09-396-196G-28315
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C 24	12.2	67.8	25	3	US-09-396-196G-50091
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C 26	12.2	67.8	25	3	US-09-396-196G-50091
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Sequence 78894, A	US-09-396-196G-78894	25	67.8	12.2	C 27
Sequence 11, Appl	US-08-726-528A-11	36	67.8	12.2	28
Sequence 719, App	US-08-974-549A-719	50	67.8	12.2	29
Sequence 719, App	US-09-721-456-719	50	67.8	12.2	30
Sequence 2189, App	US-10-131-827-2189	60	67.8	12.2	31
Sequence 720, App	US-08-974-549A-720	60	67.8	12.2	C 32
Sequence 720, App	US-09-721-456-720	60	67.8	12.2	C 33
Sequence 5, Appl	US-09-903-771-5	34	66.7	12	C 34
Sequence 44, Appl	US-08-705-477E-44	36	66.7	12	C 35
Sequence 13511, A	US-09-371-772B-13511	38	66.7	12	C 36
Sequence 18, Appl	US-08-170-095B-18	20	65.6	11.8	C 37
Sequence 18, Appl	US-08-396-866-18	20	65.6	11.8	C 38
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Sequence 41, Appl	US-09-352-654A-41	24	65.6	11.8	C 41
Sequence 41, Appl	US-09-348-097-41	24	65.6	11.8	C 42
Sequence 41, Appl	US-09-350-275-41	24	65.6	11.8	C 43
Sequence 41, Appl	US-09-909-558-41	24	65.6	11.8	C 44
Sequence 42, Appl	US-08-980-326-42	24	65.6	11.8	C 45
Sequence 19, Appl	US-07-722-798A-19	25	65.6	11.8	46
Sequence 20, Appl	US-07-722-798A-20	25	65.6	11.8	47
Sequence 124, App	US-08-271-880A-124	25	65.6	11.8	48
Sequence 124, App	US-08-271-880A-124	25	65.6	11.8	49
Sequence 147, App	US-08-910-408-124	25	65.6	11.8	50
Sequence 147, App	US-08-910-408-147	25	65.6	11.8	51
Sequence 124, App	US-09-249-215-124	25	65.6	11.8	52
Sequence 147, App	US-09-249-215-147	25	65.6	11.8	53
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Sequence 9161, Ap	US-09-396-196G-9161	25	65.6	11.8	55
Sequence 79262, A	US-09-396-196G-79262	25	65.6	11.8	56
Sequence 6, Appl	US-09-439-000-6	27	65.6	11.8	C 57
Sequence 4, Appl	US-08-952-948-4	33	65.6	11.8	C 58
Sequence 14, Appl	US-08-762-433-14	36	65.6	11.8	59
Sequence 14, Appl	US-09-001-213-14	36	65.6	11.8	60
Sequence 3, Appl	US-08-952-948-3	36	65.6	11.8	61
Sequence 6, Appl	US-09-598-218-6	36	65.6	11.8	62
Sequence 6, Appl	US-09-986-633A-6	36	65.6	11.8	63
Sequence 6, Appl	US-09-986-667A-6	36	65.6	11.8	64
Sequence 6, Appl	US-09-986-668A-6	36	65.6	11.8	65
Sequence 17, Appl	US-08-723-306-17	40	65.6	11.8	66
Sequence 2, Appl	PCT-US96-10041-17	46	65.6	11.8	C 67
Sequence 17, Appl	US-08-790-963-58	46	65.6	11.8	68
Sequence 58, Appl	US-09-371-774-58	46	65.6	11.8	C 69
Sequence 58, Appl	US-09-875-082-58	46	65.6	11.8	C 70
Sequence 2273, Ap	US-09-422-978-2273	47	65.6	11.8	C 71
Sequence 4667, Ap	US-10-131-827-4667	50	65.6	11.8	C 72
Sequence 57, Appl	US-08-418-848A-57	54	65.6	11.8	73
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Sequence 57, Appl	US-08-790-963-57	70	65.6	11.8	79
Sequence 57, Appl	US-09-371-774-57	70	65.6	11.8	80
Sequence 57, Appl	US-09-875-082-57	70	65.6	11.8	81
Sequence 118, App	US-09-166-186-118	70	64.4	11.6	C 82
Sequence 118, App	US-09-313-932-118	20	64.4	11.6	C 83
Sequence 37, Appl	US-08-158-189-37	24	64.4	11.6	C 84
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Sequence 42755, A	US-09-396-196G-42755	25	64.4	11.6	C 86
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Sequence 67783, A	US-09-396-196G-67783	25	64.4	11.6	C 88
Sequence 82076, A	US-09-396-196G-82076	25	64.4	11.6	C 89
Sequence 86954, A	US-09-396-196G-86954	25	64.4	11.6	C 90
Sequence 86260, A	US-09-396-196G-86260	25	64.4	11.6	91
Sequence 110554, A	US-09-396-196G-110554	25	64.4	11.6	C 92
Sequence 38, Appl	US-09-471-573A-38	32	64.4	11.6	93
Sequence 4, Appl	US-09-829-631A-4	33	64.4	11.6	C 94
Sequence 58, Appl	US-08-779-113-58	37	64.4	11.6	C 95
Sequence 1029, Ap	US-09-443-199C-1029	51	64.4	11.6	C 96
Sequence 1030, Ap	US-09-443-199C-1030	51	64.4	11.6	C 97

98 11.6 64.4 55 3 US-08-956-171E-2263 Sequence 2263, Ap  
 99 11.6 64.4 55 3 US-08-781-986A-2263 Sequence 2263, Ap  
 c 100 11.4 63.3 15 2 US-08-456-840-33 Sequence 33, Appl

# ALIGNMENTS

RESULT 1  
 US-09-657-042A-36/c  
 ; Sequence 36, Application US/09657042A  
 ; Patent No. 6329203  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Jacqueline Wyatt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION  
 ; FILE REFERENCE: RTS-0148  
 ; CURRENT APPLICATION NUMBER: US/09/657,042A  
 ; CURRENT FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 88  
 ; SEQ ID NO 36  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-657-042A-36

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 Db 18 GCCTTGAGAACTTCAGG 2

RESULT 2  
 US-10-131-827-8979  
 ; Sequence 8979, Application US/10131827  
 ; Patent No. 6905827  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fty, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
 ; FILE REFERENCE: 50661200120  
 ; CURRENT APPLICATION NUMBER: US/10/131,827  
 ; CURRENT FILING DATE: 2002-09-06  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 9090  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8979  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer  
 US-10-131-827-8979

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 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
 Db 3 TGCCTTGAGAACTTCGAG 20

RESULT 3  
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 ; Sequence 1069, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1069  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-396-196G-1069

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 Best Local Similarity 83.3%; Pred. No. 9.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18  
 Db 19 TGCCTTGAGAACTTCGAG 2

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 ; Sequence 54888, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 54888  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-09-396-196G-54888

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 Best Local Similarity 83.3%; Pred. No. 9.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 20 TGCCTTGAGAACTTCGAG 3

RESULT 5  
 US-09-396-196G-68119  
 ; Sequence 68119, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart

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; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 1272
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 694
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 2 of 2 allelic variants (693 is other entry)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43054295
US-09-443-199C-694

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Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

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RESULT 8
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; Sequence 5, Application US/09998547
; Patent No. 6716813
; GENERAL INFORMATION:
; APPLICANT: Lim, David J.
; APPLICANT: Lee, Haa-Yung
; APPLICANT: Webster, Paul
; APPLICANT: Andalibi, Ali
; APPLICANT: Li, Jian-Dong
; APPLICANT: Ganz, Tomas
; TITLE OF INVENTION: USE OF ANTIMICROBIAL PROTEINS AND
; TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT OF OTITIS MEDIA
; FILE REFERENCE: HOUSE1.002A
; CURRENT APPLICATION NUMBER: US/09/998,547
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/253,492
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: human beta-defensin-1 forward primer.
US-09-998-547-5

Query Match          69.8%; Score 12.4; DB 3; Length 22;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0;

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DB      2  GCCATGAGAACTTC 15

RESULT 9
US-09-396-196G-54889/c
; Sequence 54889, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart

```

; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 54889  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-54889

Query Match 68.9%; Score 12.4; DB 3; Length 25;  
Best Local Similarity 92.9%; Pred. No. 2.6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14  
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Db 14 TGCCTTGAGAACTT 1

RESULT 10  
US-09-396-196G-75625/c  
; Sequence 75625, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 75625  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-75625

Query Match 68.9%; Score 12.4; DB 3; Length 25;  
Best Local Similarity 92.9%; Pred. No. 2.6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTCGG 17  
|||||  
Db 23 CTTGAGAACTTAGG 10

RESULT 11  
US-09-396-196G-75626/c  
; Sequence 75626, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 75626  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-75626

Query Match 68.9%; Score 12.4; DB 3; Length 25;  
Best Local Similarity 92.9%; Pred. No. 2.6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTCGG 17  
|||||  
Db 17 CTTGAGAACTTAGG 4

RESULT 12  
US-08-991-525B-86/c  
; Sequence 86, Application US/08991525B  
; Patent No. 6093811  
; GENERAL INFORMATION:  
; APPLICANT: Bennett and Mirabelli  
; TITLE OF INVENTION: Oligonucleotide Modulation  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Law Offices of Jane Massey Licata  
; STREET: 66 East Main Street  
; CITY: Marlton  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WORDPERFECT 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,525B  
; FILING DATE: December 16, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,740  
; FILING DATE: May 12, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 063,167  
; FILING DATE: May 17, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 969,151  
; FILING DATE: February 10, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 007,997  
; FILING DATE: January 21, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 939,855  
; FILING DATE: September 2, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 567,286  
; FILING DATE: August 14, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISPH-0247  
; TELEPHONE: (856) 810-1515  
; TELEFAX: (856) 810-1454  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: Yes  
US-08-991-525B-86



Query Match 68.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 2.7e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTCG 17  
|||||  
Db 31 CTTGAGAACTTCAG 18

RESULT 13  
US-08-456-840-11/c  
; Sequence 11, Application US/08456840  
; Patent No. 5597908  
; GENERAL INFORMATION:  
; APPLICANT: Taddei-Peters, W. C.  
; APPLICANT: Butler, Sandra M.  
; TITLE OF INVENTION: Immunoactive Peptides of Apo(a)  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akzo No. 5597908el  
; STREET: 1330 Piccard Drive  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: US  
; ZIP: 20850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,840  
; FILING DATE: 01-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/266,407  
; FILING DATE: 27-JUN-1994  
; APPLICATION NUMBER: US 08/172,461  
; FILING DATE: 21-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gormley, Mary E.  
; REGISTRATION NUMBER: 34,409  
; TELEPHONE: 301-258-5200  
; TELEFAX: 301-977-0847  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..39  
US-08-456-840-11

Query Match 68.9%; Score 12.4; DB 2; Length 39;  
Best Local Similarity 92.9%; Pred. No. 2.8e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15  
|||||  
Db 25 GCCTTGAGAACTTC 12

RESULT 14  
US-08-266-407A-11/c  
; Sequence 11, Application US/08266407A  
; Patent No. 5786156  
; GENERAL INFORMATION:

; APPLICANT: Taddei-Peters, W. C.  
; APPLICANT: Butler, Sandra M.  
; TITLE OF INVENTION: Immunoactive Peptides of Apo(a)  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akzo No. 5786156el  
; STREET: 1330 Piccard Drive  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: US  
; ZIP: 20850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/266,407A  
; FILING DATE: 27-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/172,461  
; FILING DATE: 21-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gormley, Mary E.  
; REGISTRATION NUMBER: 34,409  
; TELEPHONE: 301-258-5200  
; TELEFAX: 301-977-0847  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..39  
US-08-266-407A-11

Query Match 68.9%; Score 12.4; DB 2; Length 39;  
Best Local Similarity 92.9%; Pred. No. 2.8e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15  
|||||  
Db 25 GCCTTGAGAACTTC 12

RESULT 15  
US-08-892-544-11/c  
; Sequence 11, Application US/08892544  
; Patent No. 5874544  
; GENERAL INFORMATION:  
; APPLICANT: Taddei-Peters, W. C.  
; APPLICANT: Butler, Sandra M.  
; TITLE OF INVENTION: Immunoactive Peptides of Apo(a)  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Akzo No. 5874544el  
; STREET: 1330 Piccard Drive  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: US  
; ZIP: 20850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/892,544
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/266,407
; APPLICATION NUMBER: 27-JUN-1994
; FILING DATE: 27-JUN-1994
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..39
US-08-892-544-11

Query Match 68.9%; Score 12.4; DB 2; Length 39;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
Db 25 GCCTTGAGAACTTC 12

RESULT 16
US-07-982-712-14
; Sequence 14, Application US/07982712
; Patent No. 5436391
; GENERAL INFORMATION:
; APPLICANT: Hideya FUJIMOTO, Kimiko ITOH
; APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO
; TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
; TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/982,712
; FILING DATE: 19921127
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
```

```
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-07-982-712-14

Query Match 68.9%; Score 12.4; DB 2; Length 68;
Best Local Similarity 92.9%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCG 16
Db 21 CCTCGAGAACTTCG 34

RESULT 17
US-09-149-727-59/c
; Sequence 59, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Kilian, Andrzej
; APPLICANT: Keese, Paul Konrad
; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 190106.405
; CURRENT APPLICATION NUMBER: US/09/149,727
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: US 60/058,263
; EARLIER FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide. Product of Synthesis to Overlap
; OTHER INFORMATION: and create fragments of engineered secretatable
; OTHER INFORMATION: microbial GUS (Figure 13)
US-09-149-727-59

Query Match 68.9%; Score 12.4; DB 3; Length 80;
Best Local Similarity 92.9%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTGAGAACTTCGG 18
Db 48 TTGAGAACTTCGTG 35

RESULT 18
US-09-270-957-98/c
; Sequence 98, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENE
; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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Patent No. 6821724  
 GENERAL INFORMATION:  
 APPLICANT: Michael Mittmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G  
 CURRENT FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: 60/100,678  
 PRIOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 28317  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-09-396-196G-28317

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
 Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGGG 18  
 ||||| ||||| |||||  
 Db 6 GCCGTGACAACTTAGGG 22

RESULT 24  
 US-09-396-196G-50091  
 Sequence 50091, Application US/09396196G  
 Patent No. 6821724  
 GENERAL INFORMATION:  
 APPLICANT: Michael Mittmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G  
 CURRENT FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: 60/100,678  
 PRIOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 50091  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: mus musculus  
 US-09-396-196G-50091

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
 Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 17  
 ||||| ||||| |||||  
 Db 8 TGCCTAGAGGACTTCAG 24

RESULT 25  
 US-09-396-196G-56271  
 Sequence 56271, Application US/09396196G  
 Patent No. 6821724  
 GENERAL INFORMATION:  
 APPLICANT: Michael Mittmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: 60/100,678  
 PRIOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 56271  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: mus musculus  
 US-09-396-196G-56271  
 Query Match 67.8%; Score 12.2; DB 3; Length 25;  
 Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGGG 18  
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 Db 1 GCCTTGAGAGCTGCAGG 17

Search completed: March 3, 2006, 07:34:54  
 Job time : 24.6441 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds  
(without alignments)  
855.220 Million cell updates/sec

Title: US-10-655-801-21  
Perfect score: 18  
Sequence: 1 tgccttgagaacttgggg 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	73.3	79	9	AZ386276 IM0145109
2	13	72.2	50	1	AU108006 AU108006
3	13	72.2	57	9	AZ308357 IM0011E16
4	12.8	71.1	52	9	BZ354347 SALK_1248
5	12.8	71.1	57	4	AK203902 Mus muscu
6	12.8	71.1	61	1	AA128432 zn87h02.s
7	12.8	71.1	61	2	BG314971 OP3.0.5.H
8	12.8	71.1	63	10	BX892304 Arabidops
9	12.8	71.1	65	10	CL212445 G041A09.G
10	12.8	71.1	66	3	BM284500 K159f03.Y
11	12.8	71.1	66	3	BM517906 K184b10.Y
12	12.8	71.1	80	11	CR397183 Arabidops
13	12.4	68.9	30	9	CC883430 SALK_0942
14	12.4	68.9	33	9	BZ664879 SALK_1102
15	12.4	68.9	52	9	BH790794 SALK_0579
16	12.4	68.9	64	1	AA829832 G040C01.s
17	12.4	68.9	65	6	CD909034 G468.111J
18	12.4	68.9	73	9	BZ381796 SALK_1173
19	12.4	68.9	78	8	DR026237 Osmo00105
20	12.2	67.8	49	1	AI528848 ms21h05.x
21	12.2	67.8	49	1	AA561711 vl35e04.r
22	12.2	67.8	54	11	CR022666 Reverse s

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c 96 11.2 62.2 51 8 DN603727 ACAC-aabs
97 11.2 62.2 55 9 CC887614 SALK 1504
98 11.2 62.2 57 5 BX723374 BX723374
99 11.2 62.2 58 1 AA935194 ny39b06.s
c 100 11.2 62.2 59 3 BM176238 T9ESTzby2

ALIGNMENTS

RESULT 1
AZ386276 79 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION
IM0145109F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0145109 F, genomic survey sequence.
ACCESSION
AZ386276
VERSION
AZ386276.1 GI:10499976
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 79)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: I column: 09
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 79.
FEATURES
source
Location/Qualifiers
1..79
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0145109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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ORIGIN
Query Match 73.3%; Score 13.2; DB 9; Length 79;
Best Local Similarity 83.3%; Pred. No. 4.le+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
|||||
Db 29 TGCCAGGAGAACTTCGGG 46

RESULT 2
AZ308357 57 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM0011E16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0011E16 F, genomic survey sequence.
ACCESSION
AZ308357
VERSION
AZ308357.1 GI:10348269
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 57)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Oca,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP16515"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 72.2%; Score 13; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTT 14
|||||
Db 14 GCCTTGAGAACTT 26

RESULT 3
AZ308357 57 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM0011E16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0011E16 F, genomic survey sequence.
ACCESSION
AZ308357
VERSION
AZ308357.1 GI:10348269
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 57)

```

**AUTHORS**  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL**  
Unpublished (2000)

**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0011 row: E column: 16  
Seq primer: CGTTGTAAACGACGGCCACT  
Class: plasmid ends  
High quality sequence stop: 57.

**FEATURES**  
Location/Qualifiers  
1..57  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0011E16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORIGIN**  
Query Match 72.2%; Score 13; DB 9; Length 57;  
Best Local Similarity 100.0%; Pred. No. 4.9e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**  
1 TGCCTTGAGAACT 13  
|||||

**Db**  
27 TGCCTTGAGAACT 39

**RESULT 4**  
BZ354347

**LOCUS**  
SALK\_124807.28.30.x Arabidopsis thaliana TDNA insertion lines

**DEFINITION**  
Arabidopsis thaliana genomic clone SALK\_124807.28.30.x, genomic survey sequence.

**ACCESSION**  
BZ354347

**VERSION**  
BZ354347.1 GI:24945209

**KEYWORDS**  
GSS.

**SOURCE**  
Arabidopsis thaliana (thale cress)

**ORGANISM**  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

**REFERENCE**  
1 (bases 1 to 52)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Cadriab, C., Karnes, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@alk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g07170.  
Class: TDNA tagged.

**FEATURES**  
Location/Qualifiers  
1..52  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_124807.28.30.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna\_protocols.html"

**ORIGIN**  
Query Match 71.1%; Score 12.8; DB 9; Length 52;  
Best Local Similarity 87.5%; Pred. No. 6.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY**  
1 TGCCTTGAGAACTTCG 16  
|||||

**Db**  
24 TCCCTTGAGAAATTCG 39

**RESULT 5**  
AK203902/c

**LOCUS**  
AK203902  
Mus musculus cDNA, clone: Y1G0146J21, strand: plus,  
reference: ENSEMBL: Mouse-Transcript-ENST: ENSMUST00000067124, based on BLAT search.

**ACCESSION**  
AK203902

**VERSION**  
AK203902.1 GI:56028079

**KEYWORDS**  
HTC; ASSETS.

**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
1  
Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y., and Carninci, P.  
Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas  
Nat. Methods 1, 233-239 (2004)  
2 (bases 1 to 57)  
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A., and Hayashizaki, Y.  
Direct Submission  
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

**rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.**

**REFERENCE**  
1 (bases 1 to 52)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Cadriab, C., Karnes, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@alk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g07170.  
Class: TDNA tagged.

**FEATURES**  
Location/Qualifiers  
1..52  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_124807.28.30.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna\_protocols.html"

**ORIGIN**  
Query Match 71.1%; Score 12.8; DB 9; Length 52;  
Best Local Similarity 87.5%; Pred. No. 6.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY**  
1 TGCCTTGAGAACTTCG 16  
|||||

**Db**  
24 TCCCTTGAGAAATTCG 39

**RESULT 5**  
AK203902/c

**LOCUS**  
AK203902  
Mus musculus cDNA, clone: Y1G0146J21, strand: plus,  
reference: ENSEMBL: Mouse-Transcript-ENST: ENSMUST00000067124, based on BLAT search.

**ACCESSION**  
AK203902

**VERSION**  
AK203902.1 GI:56028079

**KEYWORDS**  
HTC; ASSETS.

**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
1  
Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y., and Carninci, P.  
Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas  
Nat. Methods 1, 233-239 (2004)  
2 (bases 1 to 57)  
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A., and Hayashizaki, Y.  
Direct Submission  
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

**COMMENT**  
Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFLCI vector. (Reference).

**FEATURES****source**

1..57  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="Y1G0146J21"  
/cell\_line="mixture of B16-F10Y and melan-c"  
/cell\_type="mixture of melanoma cell and melanocyte cell"  
/clone\_lib="Alternative Splicing Library Li"  
/note="strand:plus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000067124, based on BLAT search"

**ORIGIN**

**Query Match** 71.1%; Score 12.8; DB 4; Length 57;  
**Best Local Similarity** 87.5%; Pred. No. 6.3e+04;  
**Matches** 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**Qy** 2 GCCTTGAGAACTTCGG 17  
||||| |||||  
**Db** 40 GCCTTGAGCTCTTCGG 25

**RESULT 6****AA128432****LOCUS**

**DEFINITION** z887h02.81 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565203 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1]; mRNA sequence.

**ACCESSION****VERSION****KEYWORDS****SOURCE****ORGANISM**

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE****AUTHORS**

1 (bases 1 to 61)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Warra, M.

**TITLE** Generation and analysis of 280,000 human expressed sequence tags  
**JOURNAL** Genome Res. 6 (9), 807-828 (1996)  
**PUBMED** 8889549

**COMMENT**

Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
Insert Length: 534 Std Error: 0.00  
Seq primer: -40M13 fwd. from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

**FEATURES****source**

1..61  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:4594268"  
/db\_xref="taxon:9606"  
/clone="IMAGE:565203"  
/tissue\_type="lung carcinoma"  
/cell\_line="NCI-H69"  
/dev\_stage="cell line NCI-H69"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="Stratagene lung carcinoma 937218"  
/notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Small cell carcinoma cell line NCI-H69. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

**ORIGIN**

**Query Match** 71.1%; Score 12.8; DB 1; Length 61;  
**Best Local Similarity** 87.5%; Pred. No. 6.4e+04;  
**Matches** 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**Qy** 2 GCCTTGAGAACTTCGG 17  
||||| |||||

**Db** 42 GCCTTGATTAACCTCGG 57

**RESULT 7****BG314971/c****LOCUS****DEFINITION**

OP3.0.5 Human THP1 cell line library Homo sapiens cDNA, mRNA sequence.

**ACCESSION****VERSION****KEYWORDS****SOURCE****ORGANISM**

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE****AUTHORS**

1 (bases 1 to 61)  
Andersson, T., Borang, S., Larsson, M., Thelin, A., Ekstrand-Hammarstrom, B., Wirta, V., Wenborg, A., Lundberg, J. and Odeberg, J.

**TITLE** Identification of candidate genes in atherosclerosis - Virtual chip analysis in RDA based transcript profiling of monocyte/macrophage response to oxidised LDL

**JOURNAL****COMMENT**

Contact: Andersson Tove  
Department of Biotechnology  
KTH  
Teknikringen 34, plan 6, 100 44 Stockholm, Sweden  
Tel: +46 8 790 71 29  
Fax: +46 8 245452  
Email: tove@biochem.kth.se  
POLYA-No.

**FEATURES****source**

1..61  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="THP1"  
/clone\_lib="Human THP1 cell line library"

/note="Vector: pRIT28; Site 1: BamHI; Site 2: BamHI; Shotgun cloning of RDA difference products. Macrophage and foamcell libraries were submitted to successive rounds of subtractive hybridisations generating populations of gene fragments that are differentially expressed in macrophage to foam cell formation."

**ORIGIN**

**Query Match** 71.1%; Score 12.8; DB 2; Length 61;



Query Match 71.1%; Score 12.8; DB 10; Length 63;

SOURCE	Ascaris suum (pig roundworm)
ORGANISM	Ascaris suum

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;  
Ascaridoidea; Ascarididae; Ascaris.

1 (bases 1 to 66)

REFERENCE  
AUTHORS  
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Claire Murphy, Brandi Chiapelli, and  
Dr. James McCarter at Washington University, St. Louis. DNA  
Sequencing by: Washington University Genome Sequencing Center  
Seq primer: -40RP from Gibco.

FEATURES  
source  
1..66  
/organism="Ascaris suum"  
/mol\_type="mRNA"  
/db\_xref="taxon:6253"  
/sex="Male"  
/tissue\_type="Intestine"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="Ascaris suum male gut SL1 TOPO v1 Murphy  
Chiapelli McCarter"  
/notes="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;  
Site 2: EcoRI; The library was constructed by Claire  
Murphy, Brandi Chiapelli, and Dr. James McCarter at  
Washington University, St. Louis. Oligo(dT)-SL1 PCR based  
library. Ascaris suum male intestine cDNA PCR products of  
size >400 nucleotides containing SL1 on the 5' end and  
oligo(dT) on the 3' end were non-directionally cloned  
into pCRII-TOPO(Invitrogen) following the Topo TA cloning  
protocol. Dissected nematode tissues were provided by Dr.  
Alan Scott (ascott@jhph.edu) of the School of Public  
Hygiene and Public Health at John Hopkins University in  
Baltimore, MD"

ORIGIN  
Query Match 71.1%; Score 12.8; DB 3; Length 66;  
Best Local Similarity 87.5%; Pred. No. 6.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCG 16  
|||||  
Db 43 TGCCTTGAGAAAGTTG 28

RESULT 11  
BM517906/c  
LOCUS  
DEFINITION  
BM517906 66 bp mRNA linear EST 15-FEB-2002  
McCarter Ascaris suum male head SL1 TOPO v1 Murphy Chiapelli  
BM517906  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Ascaris suum (pig roundworm)  
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;  
Ascaridoidea; Ascarididae; Ascaris.

REFERENCE  
AUTHORS  
1 (bases 1 to 66)  
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Claire Murphy, Brandi Chiapelli, and  
Dr. James McCarter at Washington University, St. Louis. DNA  
Sequencing by: Washington University Genome Sequencing Center  
Seq primer: -40RP from Gibco.

FEATURES  
source  
1..66  
/organism="Ascaris suum"  
/mol\_type="mRNA"  
/db\_xref="taxon:6253"  
/sex="Male"  
/tissue\_type="Head"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="Ascaris suum male head SL1 TOPO v1 Murphy  
Chiapelli McCarter"  
/notes="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;  
Site 2: EcoRI; The library was constructed by Claire  
Murphy, Brandi Chiapelli, and Dr. James McCarter at  
Washington University, St. Louis. Oligo(dT)-SL1 PCR based  
library. Ascaris suum male head cDNA PCR products of size  
>400 nucleotides containing SL1 on the 5' end and  
oligo(dT) on the 3' end were non-directionally cloned  
into pCRII-TOPO(Invitrogen) following the Topo TA cloning  
protocol. Dissected nematode tissues were provided by Dr.  
Alan Scott (ascott@jhph.edu) of the School of Public  
Hygiene and Public Health at John Hopkins University in  
Baltimore, MD."

ORIGIN  
Query Match 71.1%; Score 12.8; DB 3; Length 66;  
Best Local Similarity 87.5%; Pred. No. 6.5e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCG 16  
|||||  
Db 43 TGCCTTGAGAAAGTTG 28

RESULT 12  
CR397183  
LOCUS  
DEFINITION  
CR397183 80 bp DNA linear GSS 02-MAY-2004  
Arabidopsis thaliana T-DNA flanking sequence GK-414H01-026070,  
genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
1  
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.  
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)  
12874060  
2  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and

**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**REFERENCE**  
**AUTHORS**  
**JOURNAL**  
**COMMENT**

Weishaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
 flanking sequence tag-based reverse Genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321  
 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and  
 Weishaar, B.  
 High-throughput generation of sequence indexes from T-DNA  
 mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050  
 4 (bases 1 to 80)  
 Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.  
 Direct Submission  
 Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer  
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA.  
 It indicates an insertion close to or within gene At3g22690.  
 Details on the protocols used for generation of the sequence are  
 described in References 1-3. The sequences are generated at the MPI  
 for Plant Breeding Research in the context of the GABI-Kat project.  
 GABI-Kat is part of the German Plant Genomics program designated  
 'GABI'. Information on line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

# **FEATURES** **source**

1. .80  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161 (GenBank accession number: AJ537514). The  
 lines contain one or more T-DNA insertions. The DNA  
 fragment(s) resulting from the PCR were directly sequenced  
 to determine the genomic sequence flanking the insertion.  
 T-DNA derived sequences were removed."

## **ORIGIN**

Query Match 71.1%; Score 12.8; DB 11; Length 80;  
 Best Local Similarity 87.5%; Pred. No. 6.7e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 CCTTGAGAACTTCGGG 18  
 Db 21 CTTTGAGAACTTCGAG 36

**RESULT 13**  
**CC883430/C**  
**LOCUS**  
**DEFINITION**  
**ACCESSION**  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

CC883430 30 bp DNA linear GSS 31-JUL-2003  
 SALK\_094253.25.20.x Arabidopsis thaliana T-DNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_094253.25.20.x, genomic  
 survey sequence.  
 CC883430 GI:33359786  
 CC883430.1  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 30)  
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 Shinn, P., Zimmerman, J. and Ecker, J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker

# **FEATURES** **source**

1. .30  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more T-DNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"

## **ORIGIN**

Query Match 68.9%; Score 12.4; DB 9; Length 30;  
 Best Local Similarity 92.9%; Pred. No. 9.4e+04;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TGCCTTGAGAACTT 14  
 Db 23 TGCCTTGAGAACTT 10

## **RESULT 14** **BZ664879** **LOCUS** **DEFINITION**

BZ664879 33 bp DNA linear GSS 31-JAN-2003  
 SALK\_110222.24.20.x Arabidopsis thaliana T-DNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_110222.24.20.x, genomic  
 survey sequence.  
 BZ664879 GI:28181941  
 BZ664879.1  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 33)  
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 Shinn, P., Zimmerman, J. and Ecker, J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker

## **TITLE** **JOURNAL** **COMMENT**

The Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 T-DNA.  
 Class: T-DNA tagged.

# **FEATURES** **source**

1. .33  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 T-DNA. This sequence lies within an annotated exon of At3g51570.  
 Class: T-DNA tagged.

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 33;  
Best Local Similarity 92.9%; Pred. No. 9.5e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTGAGAACTTCGGG 18  
|||||

Db 5 TTAAGAACTTCGGG 18  
|||||

## RESULT 15

BH790794

LOCUS

DEFINITION SALK\_057921.45.15.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_057921.45.15.x, genomic survey sequence.

ACCESSION BH790794.1 GI:19883892

VERSION BH790794

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 52)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

JOURNAL Unpublished (2001)

COMMENT Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of Atlg20850.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers  
1..52  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_057921.45.15.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 52;  
Best Local Similarity 92.9%; Pred. No. 1e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTTTGAAGAACTTCG 16  
|||||

Db 3 CTTTGAAGAACTTCG 16  
|||||

## RESULT 16

AA829832/c

LOCUS

DEFINITION

AA829832.1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1370400 3',

mrna sequence.

ACCESSION AA829832

VERSION AA829832.1 GI:2902931

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 64)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,

Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 957 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 53.

Location/Qualifiers

1..64

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="taxon:9606"

/clone="IMAGE:1370400"

/tissue\_type="germinal center B cell"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GCB1"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker: Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3'

]. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 68.9%; Score 12.4; DB 1; Length 64;

Best Local Similarity 92.9%; Pred. No. 1.1e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTC 15  
|||||

Db 58 GCCTTGAGAACTTC 45  
|||||

## RESULT 17

CD909034

LOCUS

DEFINITION

G468.111J08F010817 G468 Triticum aestivum cDNA clone G468111J08,

mrna sequence.

ACCESSION CD909034

VERSION CD909034.1 GI:32683358

KEYWORDS EST.

SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.  
REFERENCE  
1 (bases 1 to 65)  
AUTHORS  
Genoplante.  
TITLE  
Genoplante, a major partnership french program in plant genomics  
JOURNAL  
Unpublished (2003)  
COMMENT  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES  
source  
1..65  
Location/Qualifiers  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="recital"  
/db\_xref="taxon:4565"  
/clone="G468111J08"  
/tissue\_type="grain (468 degrees per day after pollination)"  
/clone\_lib="G468"

ORIGIN  
Query Match 68.9%; Score 12.4; DB 6; Length 65;  
Best Local Similarity 92.9%; Pred. No. 1.1e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTGAGAACTTCGGG 18  
|||||  
Db 43 TTGAGTACTTCGGG 56  
|||||

RESULT 18  
BZ381796  
LOCUS  
SALK\_117315.18.95.n Arabidopsis thaliana TDNA insertion lines  
DEFINITION  
Arabidopsis thaliana genomic clone SALK\_117315.18.95.n, genomic survey sequence.  
ACCESSION  
BZ381796  
VERSION  
BZ381796.1 GI:25476104  
KEYWORDS  
GSS.  
SOURCE  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 (bases 1 to 73)  
AUTHORS  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
TITLE  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [ecker@salk.edu](mailto:ecker@salk.edu)  
This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1..73  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"

FEATURES  
source  
1..73  
Location/Qualifiers  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:186039"  
/clone="FCyleSTa35b04.s1"  
/clone\_lib="F. cyindrus osmotic stress library"  
/note="Samples for total RNA isolation were taken continuous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraction was performed with RNeasy (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Cloneminer Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

ORIGIN  
Query Match 68.9%; Score 12.4; DB 8; Length 78;  
Best Local Similarity 92.9%; Pred. No. 1.1e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14

/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_117315.18.95.n"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN  
Query Match 68.9%; Score 12.4; DB 9; Length 73;  
Best Local Similarity 92.9%; Pred. No. 1.1e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCG 16  
|||||  
Db 41 CCTTGAGAACTTTG 54  
|||||

RESULT 19  
DR026237/c  
LOCUS  
DEFINITION  
Osm000105 F. cyindrus osmotic stress library Fragilariopsis  
cyindrus cDNA clone FCyleSTa35b04.s1, mRNA sequence.  
ACCESSION  
DR026237  
VERSION  
DR026237.1 GI:66748600  
KEYWORDS  
EST  
SOURCE  
Fragilariopsis cyindrus  
Fragilariopsis cyindrus  
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.  
REFERENCE  
1 (bases 1 to 78)  
AUTHORS  
Krell,A. and Gloeckner,G.  
TITLE  
Analysis of an osmotic stress induced cDNA library of the psychrophilic diatom Fragilariopsis cylindrus  
JOURNAL  
Unpublished (2004)  
COMMENT  
Contact: Krell, Andreas; Gloeckner, Gernot  
Biological Oceanography, Sea ice research; Genome Analysis  
Alfred-Wegner-Institute for Polar and Marine Research; Institute for Molecular Biotechnology  
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr. 11, D-07745 Jena, Germany  
Tel: ++49 471 48311812; ++49 3641 656440  
Fax: ++49 471 48311425; ++49 3641 656255  
Email: [akrell@awi-bremerhaven.de](mailto:akrell@awi-bremerhaven.de); [gernot@imb-jena.de](mailto:gernot@imb-jena.de)  
PCR Primers  
FORWARD: 5'M13  
BACKWARD: 3'M13  
Seq primer: 5'GTAAACGACGGCCAG 3'.  
Location/Qualifiers  
1..78  
/organism="Fragilariopsis cylindrus"  
/mol\_type="mRNA"  
/db\_xref="taxon:186039"  
/clone="FCyleSTa35b04.s1"  
/clone\_lib="F. cyindrus osmotic stress library"  
/note="Samples for total RNA isolation were taken continuous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraction was performed with RNeasy (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Cloneminer Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

ORIGIN  
Query Match 68.9%; Score 12.4; DB 8; Length 78;  
Best Local Similarity 92.9%; Pred. No. 1.1e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14

```

Db          69  TGTCTTGAGAACTT 56
|| |||||
|| |||||

RESULT 20
AI528848
LOCUS
DEFINITION
    ma21h05.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
    IMAGE:607641 3' similar to SW:SPCO_MOUSE Q62261 SPECTRIN BETA
    CHAIN, BRAIN ;, mRNA sequence.

ACCESSION
AI528848
VERSION
AI528848.1 GI:4442983
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
FEATURES
    Location/Qualifiers
    1..49
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:607641"
    /sex="females"
    /tissue_type="whole skin"
    /dev_stage="11 weeks old"
    /lab_host="SOLR (kanamycin resistant)"
    /clone_lib="Stratagene mouse skin (#937313)"
    /note="Organ: skin; Vector: pBluescript SK-; Site 1:
    EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
    Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
    Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
    adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
    sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
ORIGIN
Query Match 67.8%; Score 12.2; DB 1; Length 49;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 17
| |||||
Db 27 TCCCTTGAGAACTGTGG 43
| |||||

RESULT 21
AA561711
LOCUS
DEFINITION
    v135e04.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
    IMAGE:974238 5' similar to SW:CPG1_RAT P10610 CYTOCHROME P450 IIG1
    ;, mRNA sequence.
    AA561711
ACCESSION
AA561711
VERSION
AI528848.1 GI:4442983
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 54)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
FEATURES
    Location/Qualifiers
    1..49
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:607641"
    /sex="females"
    /tissue_type="whole skin"
    /dev_stage="11 weeks old"
    /lab_host="SOLR (kanamycin resistant)"
    /clone_lib="Stratagene mouse skin (#937313)"
    /note="Organ: skin; Vector: pBluescript SK-; Site 1:
    EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
    Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
    Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
    adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
    sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
ORIGIN
Query Match 67.8%; Score 12.2; DB 1; Length 49;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 17
| |||||
Db 27 TCCCTTGAGAACTGTGG 43
| |||||

RESULT 22
CR022666
LOCUS
DEFINITION
    Reverse strand read from insert in 5'HPRT insertion targeting and
    chromosome engineering clone MHPN414915, genomic survey sequence.
    CR022666
ACCESSION
CR022666.1 GI:49755721
VERSION
GSS; genome survey sequence; MICR.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 54)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,

```

Rogers, J. and Bradley, A.  
 Direct Submission  
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>  
 Location/Qualifiers  
 1..54  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="WHPN414g15"  
 /clone\_lib="WHPN"

ORIGIN  
 Query Match 67.8%; Score 12.2; DB 11; Length 54;  
 Best Local Similarity 82.4%; Pred. No. 1.3e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCTTGAGAACTTCGG 17  
 Db 30 TTCTTGAGAACTTCGG 46

RESULT 23  
 CW187237  
 LOCUS 73 bp DNA linear GSS 30-OCT-2004  
 DEFINITION 104\_605\_11166986\_116\_36720\_007 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11166986, genomic survey sequence.  
 ACCESSION CW187237  
 VERSION CW187237  
 KEYWORDS GSS.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 REFERENCE 1 (bases 1 to 73)  
 AUTHORS Jones, J.A., Budman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holuman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddalo, J.A. and Martienssen, R.A.  
 SORGHUM genome sequencing by methylation filtration  
 PLoS Biol. 3 (1), e13 (2005)  
 15660154  
 CONTACT: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: 605 row: j column: 02  
 Seq primer: T3 Reverse  
 Class: methylation filtered  
 High quality sequence scop: 73.  
 Location/Qualifiers  
 1..73  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="Atx623"  
 /db\_xref="taxon:4558"  
 /clone="11166986"  
 /clone\_lib="Sorghum methylation filtered library (LibID: 104)"  
 /note="Organ: leaf; Vector: pBCK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN  
 Query Match 67.8%; Score 12.2; DB 10; Length 73;

Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCTTGAGAACTTCGG 17  
 Db 41 TGCTTGAGAACTTCGG 57

RESULT 24  
 BX949767  
 LOCUS 48 bp DNA linear GSS 05-APR-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-803A08-023416, genomic survey sequence.  
 ACCESSION BX949767  
 VERSION BX949767.1 GI:42599453  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 REFERENCE 1  
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 12874060  
 REFERENCE 2  
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321  
 REFERENCE 3  
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050  
 REFERENCE 4 (bases 1 to 48)  
 AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.  
 Direct Submission  
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g49650. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
 Location/Qualifiers  
 1..48  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-803A08-023416"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotyped="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN  
 Query Match 66.7%; Score 12; DB 10; Length 48;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTC 15  
|||||  
Db 17 CTTGAGAACTTC 28

## RESULT 25

CN544831/c

## LOCUS

## DEFINITION

70 bp mRNA linear EST 29-APR-2004  
EST0003 Apple developing fruit differentially expressed cDNA  
library Malus x domestica cDNA 5' similar to drought-stressed  
related, mRNA sequence.

## ACCESSION

CN544831

## VERSION

1

## KEYWORDS

EST.

## SOURCE

Malus x domestica

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

## REFERENCE

1 (bases 1 to 70)

## AUTHORS

Lin, S.F., Coleman, G.D. and Walsh, C.S.

## TITLE

Transcript profiling the mechanism of transition from maturation to  
ripening of 'Gala' and 'Fuji' apples

## JOURNAL

Unpublished (2004)

## COMMENT

Contact: Lin, Shu-fei  
Department of Natural Resource Sciences and Landscape Architecture  
University of Maryland College Park  
2102 Plant Sciences Building, College Park, MD 20742, USA  
Tel: 301 405 4367  
Fax: 301 314 9308  
Email: shufei@wam.umd.edu

## CDNA-AFLP

Seq primer: M13-21  
High quality sequence stop: 70

## POLYA-No.

Location/Qualifiers

1..70

/organism="Malus x domestica"

/mol\_type="mRNA"

/cultivar="Gala"

/db\_xref="taxon:3750"

/tissue\_type="Hypanthium tissue"

/dev\_stage="immature"

/clone\_lib="Apple developing fruit differentially  
expressed cDNA library"

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 70;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTC 15

|||||

Db 40 CTTGAGAACTTC 29

Search completed: March 3, 2006, 11:01:35

Job time : 990.737 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds  
(without alignments)  
2714.499 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18  
Sequence: 1 tgcacttatctggatt 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	74.4	46	8	HSLAS73A
2	13.4	74.4	60	6	CQ542438
3	13.2	73.3	21	6	AX837834
4	13.2	73.3	26	6	A21788
5	13.2	73.3	48	6	AX925501
6	13.2	73.3	48	6	AX925502
7	13.2	73.3	65	6	CQ555999
8	13.2	73.3	77	6	CQ742818
9	13.2	73.3	80	10	BX294558
10	13	72.2	20	6	CQ945532
11	12.8	71.1	19	6	AR573430
12	12.8	71.1	19	6	AR573431
13	12.8	71.1	19	6	AX131540
14	12.8	71.1	19	6	AX131541
15	12.8	71.1	24	6	AX321460
16	12.8	71.1	27	6	AR448509
17	12.8	71.1	27	6	AX255427
18	12.8	71.1	47	6	AR291139
					X91571 H.sapiens D
					CQ542438 Sequence
					AX837834 Sequence
					A21788 SEQ ID NO:
					AX925501 Sequence
					AX925502 Sequence
					CQ555999 Sequence
					CQ742818 Sequence
					BX294558 Arabidops
					CQ945532 Sequence
					AR573430 Sequence
					AR573431 Sequence
					AX131540 Sequence
					AX131541 Sequence
					AX321460 Sequence
					AR448509 Sequence
					AX255427 Sequence
					AR291139 Sequence

c	19	12.8	71.1	51	6	AX427630	AX427630 Sequence
c	20	12.8	71.1	54	6	AX427632	AX427632 Sequence
c	21	12.8	71.1	65	6	CQ534533	CQ534533 Sequence
c	22	12.8	71.1	65	6	AX484056	AX484056 Sequence
	23	12.4	68.9	15	6	A11087	A11087 Oligonucleo
	24	12.4	68.9	15	6	AR340899	AR340899 Sequence
	25	12.4	68.9	15	6	AR362712	AR362712 Sequence
	26	12.4	68.9	21	6	CQ868436	CQ868436 Sequence
	27	12.4	68.9	21	6	CQ955649	CQ955649 Sequence
	28	12.4	68.9	23	6	CS114991	CS114991 Sequence
c	29	12.4	68.9	25	6	AX614147	AX614147 Sequence
c	30	12.4	68.9	30	6	AX207312	AX207312 Sequence
c	31	12.4	68.9	41	6	AX518625	AX518625 Sequence
c	32	12.4	68.9	41	6	AX518626	AX518626 Sequence
c	33	12.4	68.9	42	6	AR055004	AR055004 Sequence
c	34	12.4	68.9	42	6	AR156253	AR156253 Sequence
c	35	12.4	68.9	42	6	AX343177	AX343177 Sequence
c	36	12.4	68.9	47	6	E15363	E15363 Oligonucleo
c	37	12.4	68.9	47	6	AR289908	AR289908 Sequence
c	38	12.4	68.9	47	6	AR289924	AR289924 Sequence
c	39	12.4	68.9	60	6	CQ784697	CQ784697 Sequence
c	40	12.4	68.9	60	6	AX496193	AX496193 Sequence
c	41	12.4	68.9	63	6	BD035124	BD035124 Sequence
c	42	12.4	68.9	63	6	AX899591	AX899591 Sequence
c	43	12.4	68.9	65	6	CQ531358	CQ531358 Sequence
c	44	12.2	67.8	21	6	E395016	E395016 Sequence 22
c	45	12.2	67.8	21	6	E38368	E38368 Binding par
c	46	12.2	67.8	21	6	E39012	E39012 Nucleic aci
c	47	12.2	67.8	21	6	AX022660	AX022660 Sequence
c	48	12.2	67.8	25	6	BD245513	BD245513 Developme
c	49	12.2	67.8	25	6	CS117930	CS117930 Sequence
c	50	12.2	67.8	30	6	AR107083	AR107083 Sequence
c	51	12.2	67.8	30	6	AR107088	AR107088 Sequence
c	52	12.2	67.8	30	6	AR118363	AR118363 Sequence
c	53	12.2	67.8	30	6	AR118368	AR118368 Sequence
c	54	12.2	67.8	30	6	CQ874733	CQ874733 Sequence
c	55	12.2	67.8	30	6	CS020544	CS020544 Sequence
c	56	12.2	67.8	30	6	CS020548	CS020548 Sequence
c	57	12.2	67.8	30	6	CS070456	CS070456 Sequence
c	58	12.2	67.8	30	6	CS070461	CS070461 Sequence
c	59	12.2	67.8	30	6	CS103069	CS103069 Sequence
c	60	12.2	67.8	30	6	AR302205	AR302205 Sequence
c	61	12.2	67.8	30	6	AR302210	AR302210 Sequence
c	62	12.2	67.8	30	6	AR308644	AR308644 Sequence
c	63	12.2	67.8	30	6	AR308722	AR308722 Sequence
c	64	12.2	67.8	30	6	AR633343	AR633343 Sequence
c	65	12.2	67.8	30	6	AR633348	AR633348 Sequence
c	66	12.2	67.8	30	6	AX813365	AX813365 Sequence
c	67	12.2	67.8	30	6	AX813370	AX813370 Sequence
c	68	12.2	67.8	30	15	AJ837777	AJ837777 Arabidops
c	69	12.2	67.8	31	6	BD136169	BD136169 Vector . 9
c	70	12.2	67.8	31	6	AR635373	AR635373 Sequence
c	71	12.2	67.8	31	6	AX002799	AX002799 Sequence
c	72	12.2	67.8	31	6	AX149567	AX149567 Sequence
c	73	12.2	67.8	34	6	AX577721	AX577721 Sequence
c	74	12.2	67.8	37	6	AR591114	AR591114 Sequence
c	75	12.2	67.8	37	6	AR591115	AR591115 Sequence
c	76	12.2	67.8	37	6	AX280623	AX280623 Sequence
c	77	12.2	67.8	37	6	AX280622	AX280622 Sequence
c	78	12.2	67.8	41	6	AX516052	AX516052 Sequence
c	79	12.2	67.8	41	6	AX517111	AX517111 Sequence
c	80	12.2	67.8	41	6	AX517458	AX517458 Sequence
c	81	12.2	67.8	41	6	AX519640	AX519640 Sequence
c	82	12.2	67.8	47	6	AX066417	AX066417 Sequence
c	83	12.2	67.8	49	6	AX066418	AX066418 Sequence
c	84	12.2	67.8	50	6	AR032931	AR032931 Sequence
c	85	12.2	67.8	50	6	I29671	I29671 Sequence 54
c	86	12.2	67.8	50	6	I91345	I91345 Sequence 54
c	87	12.2	67.8	50	6	AR209595	AR209595 Sequence
c	88	12.2	67.8	50	6	AR646909	AR646909 Sequence
c	89	12.2	67.8	51	10	BV183752	BV183752 sqmml4086
c	90	12.2	67.8	53	6	AR355948	AR355948 Sequence
c	91	12.2	67.8	53	6	AR537504	AR537504 Sequence

C 92 12.2 67.8 65 6 AX483731 Sequence  
 C 93 12 66.7 21 6 AX234635 Sequence  
 C 94 11.8 65.6 17 6 AX722575 Sequence  
 C 95 11.8 65.6 17 6 AX736854 Sequence  
 C 96 11.8 65.6 20 6 122554 Sequence 42  
 C 97 11.8 65.6 20 6 147379 Sequence 42  
 C 98 11.8 65.6 21 6 A91087 Sequence 8  
 C 99 11.8 65.6 21 6 CQ778220 Sequence 8  
 C 100 11.8 65.6 21 6 AR530667 Sequence

## ALIGNMENTS

RESULT 1  
 HSLAS73A  
 LOCUS HSLAS73A 46 bp DNA linear PRI 22-APR-1996  
 DEFINITION H. sapiens DNA for loop attachment sequence (clone LAS73A).  
 ACCESSION X91571  
 VERSION X91571.1 GI:987929  
 KEYWORDS loop attachment sequence.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 46)  
 AUTHORS Jackson, D.A., Bartlett, J. and Cook, P.R.  
 TITLE Sequences attaching loops of nuclear and mitochondrial DNA to underlying structures in human cells: the role of transcription units  
 JOURNAL Nucleic Acids Res. 24 (7), 1212-1219 (1996)  
 PUBMED 8614821  
 REFERENCE 2 (bases 1 to 46)  
 AUTHORS Cook, P.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-SEP-1995) P.R. Cook, Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, UK

## FEATURES

source  
 1..46  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="LAS73A"  
 /cell\_line="HeLa"  
 /clone\_lib="DNA loop attachment sequences (LAS)"  
 misc\_feature 1..46  
 /note="DNA loop attachment site (LAS)"

## ORIGIN

Query Match 74.4%; Score 13.4; DB 8; Length 46;  
 Best Local Similarity 93.3%; Pred. No. 3.1e+04;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTCTCTGGA 15  
 |||||  
 Db 31 TGTCACTTCTCTGGA 45

RESULT 2  
 CQ542438  
 LOCUS CQ542438 60 bp DNA linear PAT 30-JAN-2004  
 DEFINITION Sequence 12073 from Patent WO0210449.  
 ACCESSION CQ542438  
 VERSION CQ542438.1 GI:41508702  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

## REFERENCE

1

AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome  
 JOURNAL Patent: WO 0210449-A 12073 07-FEB-2002;  
 Compugen Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..60  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 60;  
 Best Local Similarity 93.3%; Pred. No. 3e+04; 1; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTCTCTGGA 15  
 |||||  
 Db 38 TGTCACTTCTCTGGA 52

## RESULT 3

AX837834/c  
 LOCUS AX837834 21 bp DNA linear PAT 15-DEC-2003  
 DEFINITION Sequence 4958 from Patent EP1347046.  
 ACCESSION AX837834  
 VERSION AX837834.1 GI:39921526  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified sequences.

REFERENCE 1  
 AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and Masuho, Y.  
 TITLE Full-length cDNA sequences  
 JOURNAL Patent: EP 1347046-A 4958 24-SEP-2003;  
 Research Association for Biotechnology (JP)

## FEATURES

source  
 1..21  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"  
 /note="Description of Artificial Sequence: an artificially synthesized primer se q"

## ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 21;  
 Best Local Similarity 83.3%; Pred. No. 4.2e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTCTCTGGA 18  
 |||||  
 Db 20 TGTCACTTCTCTGGA 3

## RESULT 4

A21788  
 LOCUS A21788 26 bp DNA linear PAT 22-AUG-1994  
 DEFINITION SEQ ID NO: 4; Oligonucleotide.  
 ACCESSION A21788  
 VERSION A21788.1 GI:583664  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 26)

AUTHORS Novoa Perez, L. I., Machado Lahera, J. A., Fernandez Maso, J. R., Benitez Fuentes, J. V., Nardandi Diaz, R. E., Rodriguez Reinoso, J. L., Estrada Garcia, M. P., Garcia Suarez, J. and Herrera Martinez, L. S.  
 TITLE Method for the expression of heterologous proteins produced in fused form in E. coli, use thereof, expression vectors and

```
recombinant strains
Patent: EP 0416673-A 4 13-MAR-1991;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGATT 18
| | | | | | | | | | | | | | | |
Db 8 TATCAGTAGCTGGATT 25
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RESULT 5
LOCUS AX925501/c 48 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 2 from Patent WO02068631.
ACCESSION AX925501
VERSION AX925501.1 GI:40243764
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Shaw,K.J., Kenney,T. and Shimer,G.H.
TITLE Plasmid for insertional mutagenesis in bacteria
JOURNAL Patent: WO 02068631-A 2 06-SEP-2002;
Genome Therapeutics Corporation (US)
FEATURES
1. .48
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Primer Sequence"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 48;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGATT 18
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Db 33 TGTCACCTAACCTGGATT 16
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RESULT 6
LOCUS AX925502 48 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 3 from Patent WO02068631.
ACCESSION AX925502
VERSION AX925502.1 GI:40243767
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Shaw,K.J., Kenney,T. and Shimer,G.H.
TITLE Plasmid for insertional mutagenesis in bacteria
JOURNAL Patent: WO 02068631-A 3 06-SEP-2002;
Genome Therapeutics Corporation (US)
FEATURES
1. .48
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Primer Sequence"

ORIGIN

recombinant strains
Patent: EP 0416673-A 4 13-MAR-1991;
CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
Location/Qualifiers
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ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 48;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGATT 18
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Db 16 TGTCACCTAACCTGGATT 33
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RESULT 7
LOCUS CQ555999 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 25634 from Patent WO0210449.
ACCESSION CQ555999
VERSION CQ555999.1 GI:41522426
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 25634 07-FEB-2002;
Compugen Inc. (US)
FEATURES
1. .65
Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 3.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGATT 18
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Db 32 TGTCAGTATCTGGATT 49
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RESULT 8
LOCUS CQ742818/c 77 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 28752 from Patent WO02068579.
ACCESSION CQ742818
VERSION CQ742818.1 GI:42354141
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 28752 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
1. .77
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity 83.3%; Pred. No. 3.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 TGTCACTTATCTGGATT 18
Db 49 TGGCGCTTATCTAGATT 32

RESULT 9
BX294558 80 bp DNA linear STS 12-JUN-2003
LOCUS Arabidopsis thaliana transposon insertion STS SM_3.3096, sequence
DEFINITION tagged site..
ACCESSION BX294558
VERSION BX294558.1 GI:29125569
KEYWORDS STS; STS; sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
REFERENCE 1
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
MURPHY, G., Langham, S., LeGryse, C., Jones, J.D.G. and Bevan, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 80)
AUTHORS Clarke, J.H.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
COMMENT AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. _3 denotes a sequence derived from the 3' end of the
transposon, _5 denotes a sequence derived from the 5' end of the
transposon. BSRG GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N57469.

FEATURES
source Location/Qualifiers
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/organism="Arabidopsis thaliana"
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/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC004681"
/notes="Derived from superpool NASC code Unknown"
1..80
/standard_name="SM_3.3096"

STS
1..80
/standard_name="SM_3.3096"

ORIGIN
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Best Local Similarity 83.3%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
Db 29 TATCACTTATCTAGATAT 46

RESULT 10
CQ945532 20 bp DNA linear PAT 01-DEC-2004
LOCUS CQ945532
DEFINITION Sequence 1 from Patent WO2004099438.
ACCESSION CQ945532
VERSION CQ945532.1 GI:56294649
KEYWORDS Toxoplasma gondii
SOURCE Toxoplasma gondii
ORGANISM Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
REFERENCE 1
AUTHORS Renaut, I., Mertens, P. and Leclipteux, T.
TITLE One step oligochromatographic device and method of use
JOURNAL Patent: WO 2004099438-A 1 18-NOV-2004;

FEATURES
source Location/Qualifiers
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/organism="Toxoplasma gondii"
/mol_type="unassigned DNA"
/db_xref="taxon:5811"
/notes="N-STX1-F2 oligonucleotide probe"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTTATCTGGATT 18
Db 4 CTTATCTGGATT 16

RESULT 11
AR573430 19 bp DNA linear PAT 14-DEC-2004
LOCUS AR573430
DEFINITION Sequence 2758 from patent US 6770633.
ACCESSION AR573430
VERSION AR573430.1 GI:56574322
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: US 6770633-A 2758 03-AUG-2004;
Immusol, Inc.; San Diego, CA
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17
Db 4 GTCCTTAACTGGATT 19

RESULT 12
AR573431 19 bp DNA linear PAT 14-DEC-2004
LOCUS AR573431
DEFINITION Sequence 2759 from patent US 6770633.
ACCESSION AR573431
VERSION AR573431.1 GI:56574323
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: US 6770633-A 2759 03-AUG-2004;
Immusol, Inc.; San Diego, CA
FEATURES
source Location/Qualifiers
1..19
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/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 3 GTCCCTAACTGGATT 18

RESULT 15			
AX321460			
LOCUS	AX321460	24 bp	DNA
DEFINITION	Sequence 10 from Patent WO0190413.	linear	PAT 15-DEC-2001

ACCESSION AX321460  
VERSION AX321460.1 GI:17905447  
KEYWORDS

SOURCE	ORGANISM
synthetic construct	
synthetic construct	

REFERENCE  
AUTHORS  
Rosell, R. and Monzo, M.  
1  
other sequences; artificial sequences.

**TITLE** Method and markers for prognosticating efficacy of anticancer agents

**JOURNAL**  
Patent: WO 0190413-A 10 29-NOV-2001;  
Pristol-McGraw Smith Co. (US)

**FEATURES**

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source
1. .24
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ORIGIN

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Best Local Similarity	87.5%	Pred. No.	7e+04;
Matches	14;	Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

0v 3 TCACCTTATCTGGATT 18

[illegible]

DB / TAACCTACCGGATTT ZZ

**RESULT 16**

AR448509/c:  
LOCIS AR448509 27 bp DNA linear DAT 20-FEB-2004

DEFINITION Sequence 7 from patent US 6673567.

ACCESSION	AK448509
VERSION	AR448509.1 GI:42676997

**KEYWORDS** Unknown.  
**SOURCE** Unknown.

ORGANISM	Unknown.	Unidentified

REFERENCE

1 (bases 1 to 27)

unclassified.

AUTHORS	Sharpe, P. L. and Nagarajan, V.
TITLE	Method of determination of gene function

JOURNAL Patent: US 6673567-A 7 06-JAN-2004;  
E. I. du Pont de Nemours and Company: Wilmington, DE

FEATURES		Location/Qualifiers
1	27	

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1. 2 /
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source
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ORIGIN
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<b>Best Local Similarity</b>	<b>87.5%;</b>	<b>Pred. No. 7e+04;</b>
<b>Matches</b>	<b>14.</b>	<b>Mismatches</b>
	<b>Concomitative</b>	<b>Indels</b>
	<b>0.</b>	<b>0.</b>

Matches	14;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0
---------	-----	--------------	----	------------	----	--------	----	------	---

1 TGTCACTTATCTGGAT 16

Db 18 TTTCACCTTATCTGGTT 3

**P E T R**

RESULTS 1/  
AX255427/c

LOCUS AX255427 27 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 7 from Patent WO0171040.

AX255427	AX255427
ACCESSION	VERSION
GT.16074601	

RECEIVED 02/12/2007  
ACCEPTED 02/12/2007  
KEYWORDS



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Query Match 71.1%; Score 12.8; DB 6; Length 65;
Best Local Similarity 87.5%; Pred. No. 6.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGATT 18
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Db 2 TCACCTGCTGATT 17

RESULT 22
AX484056/c
LOCUS AX484056 65 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1356 from Patent WO02053728.
ACCESSION AX484056
VERSION AX484056.1 GI:22318408
KEYWORDS
SOURCE
ORGANISM Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlson, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 1356 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
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ORIGIN

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGATT 17
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Db 48 GTCACCTTATCTGATT 33

RESULT 23
AX1087
LOCUS AX1087 15 bp DNA linear PAT 03-DEC-1993
DEFINITION Oligonucleotide U16.
ACCESSION AX1087
VERSION AX1087.1 GI:490937
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ikehara, M. and Kida, M.
TITLE Synthetic gene for human lysozyme
JOURNAL Patent: EP 0181634-A 31 21-MAY-1986;
Takeda Chemical Industries, Ltd
FEATURES
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ORIGIN

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QY 1 TGTCACCTTATCTGG 14
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Db 1 TGTCACCTTATCTGG 14

RESULT 24
AX340899
LOCUS AX340899 15 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 26 from patent US 6573073.
ACCESSION AX340899
VERSION AX340899.1 GI:33732842
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Harris, A.
TITLE CFTR gene regulator
JOURNAL Patent: US 6573073-A 26 03-JUN-2003;
Isis Innovation Limited; Oxford;
WOX;
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Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGG 14
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Db 1 TGTCACCTTATCTGG 14

RESULT 25
AX362712
LOCUS AX362712 15 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 46 from patent US 5182195.
ACCESSION AX362712
VERSION AX362712.1 GI:34423092
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Nakahama, K., Kaisho, Y. and Yoshimura, K.
TITLE Method for increasing gene expression using protease deficient
JOURNAL Patent: US 5182195-A 46 26-JAN-1993;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;
FEATURES
    Location/Qualifiers
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    /mol_type="genomic DNA"
ORIGIN

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Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGG 14
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Db 1 TGTCACCTTATCTGG 14

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:02:58 ; Search time 117.534 Seconds  
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Title: US-10-655-801-22  
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Sequence: 1 tgtcacttctgtgattt 18  
Scoring table: IDENTITY NUC  
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Total number of hits satisfying chosen parameters: 5180220

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Post-processing: Minimum Match 0%  
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Listing first 100 summaries

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14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	18	100.0	18	AAH47978	Aah47978 Human ind
2	14	77.8	19	ADQ62106	Adq62106 Anti-NOS2
3	13.8	76.7	30	ADP16179	Adp16179 Versinia
4	13.4	74.4	25	ADP13976	Adp13976 Renal cel
5	13.4	74.4	25	ADP13977	Adp13977 Renal cel
6	13.4	74.4	41	ADL01630	Adl01630 Escherich
7	13.4	74.4	60	ABN39325	Abn39325 Human spl
8	13.2	73.3	21	ADM06273	Adm06273 Human PCR
9	13.2	73.3	45	AAC82169	Aac82169 Human ret
10	13.2	73.3	48	ABSS5303	Abss5303 PLAC prom
11	13.2	73.3	48	ABSS5302	Abss5302 Chloramph
12	13.2	73.3	65	ABNS52886	Abns52886 Mouse spl
13	13.2	73.3	75	ADP80938	Adp80938 Mouse Dna
14	13	72.2	20	ADU73604	Adu73604 Probe N-S
15	13	72.2	50	ADR70635	Adr70635 Exemplary
16	12.8	71.1	19	AAH85172	Aah85172 Cyclin G1
17	12.8	71.1	19	AAH85173	Aah85173 Cyclin G1
18	12.8	71.1	19	AAH60334	Aah60334 Cyclin G1
19	12.8	71.1	19	AAH60335	Aah60335 Cyclin G1

23	4	AAF82405	71.1	23	4	AAF82405	Aaf82405 Mealworm
24	6	AAD26335	71.1	24	6	AAD26335	Aad26335 Human bet
27	4	AAS13868	71.1	27	4	AAS13868	Aas13868 Tn5-based
41	6	ABZ48041	71.1	41	6	ABZ48041	Abz48041 Human ATP
41	6	ABZ48040	71.1	41	6	ABZ48040	Abz48040 Human ATP
47	3	AZ68526	71.1	47	3	AZ68526	Az68526 Human map
50	6	ABZ03967	71.1	50	6	ABZ03967	Abz03967 Human leu
51	6	AABK99735	71.1	51	6	AABK99735	Aabk99735 Bpmi endo
51	13	ADU24034	71.1	51	13	ADU24034	Adu24034 PCR prime
54	6	AAK99737	71.1	54	6	AAK99737	Aak99737 Bpmi endo
54	13	ADU24038	71.1	54	13	ADU24038	Adu24038 Type IIG
54	13	ADU24036	71.1	54	13	ADU24036	Adu24036 Forward P
60	14	ADZ63509	71.1	60	14	ADZ63509	Adz63509 Murine Ap
64	12	ADO05654	71.1	64	12	ADO05654	Ado05654 PCR ampli
64	12	ADO05653	71.1	64	12	ADO05653	Ado05653 PCR ampli
65	6	ABZ27409	71.1	65	6	ABZ27409	Abz27409 Candida e
65	6	ABN31420	71.1	65	6	ABN31420	Abn31420 Rat splic
79	2	AAK11606	71.1	79	2	AAK11606	Aak11606 Human bia
17	14	ADK01097	68.9	17	14	ADK01097	Adk01097 Drug-resi
21	13	ADR70371	68.9	21	13	ADR70371	Adr70371 Polioviru
22	13	ADS19213	68.9	22	13	ADS19213	Ads19213 Serine or
23	6	ABS98050	68.9	23	6	ABS98050	Abs98050 Human mul
23	11	ADM79746	68.9	23	11	ADM79746	Adm79746 Group B S
23	11	ADM79642	68.9	23	11	ADM79642	Adm79642 Group B S
23	14	AEA46753	68.9	23	14	AEA46753	Aea46753 FKBP51 SN
30	4	AAAD14231	68.9	30	4	AAAD14231	Aad14231 Synthetic
30	5	AAS06566	68.9	30	5	AAS06566	Aas06566 Mouse mic
32	14	ADM26071	68.9	32	14	ADM26071	Adm26071 Plant tri
42	2	AAT86880	68.9	42	2	AAT86880	Aat86880 Plasmid P
42	2	AAV64697	68.9	42	2	AAV64697	Aav64697 HIV anti-
42	8	AAH24709	68.9	42	8	AAH24709	Aah24709 Nucleotid
42	8	ACA74015	68.9	42	8	ACA74015	Aca74015 Hepatitis
47	6	AAV22795	68.9	47	6	AAV22795	Aav22795 Oligonuc
47	6	ABQ96308	68.9	47	6	ABQ96308	Abq96308 Tumour su
60	12	ADK19630	68.9	60	12	ADK19630	Adk19630 Anti-M2-P
63	3	AAC11379	68.9	63	3	AAC11379	Aac11379 Human sec
65	6	ABN28245	68.9	65	6	ABN28245	Abn28245 Rat splic
21	2	AAK77884	67.8	21	2	AAK77884	Aak77884 Mouse pl6
21	13	AEA65146	67.8	21	13	AEA65146	Aea65146 Human lup
21	14	ADZ99147	67.8	21	14	ADZ99147	Adz99147 Human NOT
22	10	ADG38398	67.8	22	10	ADG38398	Adg38398 PCR prime
23	10	ADB76941	67.8	23	10	ADB76941	Adb76941 Mouse CLC
23	10	ADB76939	67.8	23	10	ADB76939	Adb76939 Mouse CLC
23	12	ADI29527	67.8	23	12	ADI29527	Adi29527 Murine CL
23	12	ADJ34752	67.8	23	12	ADJ34752	Adj34752 Mouse 2-
25	3	AAA68488	67.8	25	3	AAA68488	Aaa68488 Bacteriop
25	9	ACI09914	67.8	25	9	ACI09914	Act09914 Human mic
25	9	ACK28853	67.8	25	9	ACK28853	Ack28853 Human mic
25	9	ACI51041	67.8	25	9	ACI51041	Act51041 Human mic
27	10	ABZ80482	67.8	27	10	ABZ80482	Abz80482 Human imm
30	2	AAZ08106	67.8	30	2	AAZ08106	Aaz08106 3'RT-PCR
30	2	AAZ08111	67.8	30	2	AAZ08111	Aaz08111 PCR prime
30	3	AAA30747	67.8	30	3	AAA30747	Aaa30747 Human GPC
30	3	AAA30668	67.8	30	3	AAA30668	Aaa30668 Human G p
30	4	AAF32187	67.8	30	4	AAF32187	Aaf32187 Human oes
30	5	AAC82810	67.8	30	5	AAC82810	Aac82810 Human ser
30	5	AAC82815	67.8	30	5	AAC82815	Aac82815 Human ser
30	10	ADC22639	67.8	30	10	ADC22639	Adc22639 Human G p
30	10	ADH14228	67.8	30	10	ADH14228	Adh14228 Human G p
30	10	ADH14112	67.8	30	10	ADH14112	Adh14112 Human ser
30	12	ADI24561	67.8	30	12	ADI24561	Adi24561 Human SHT
30	12	ADI24556	67.8	30	12	ADI24556	Adi24556 Human SHT
30	13	ADR99761	67.8	30	13	ADR99761	Adr99761 Nucleic a
30	14	ADK02766	67.8	30	14	ADK02766	Adk02766 Human 5-H
30	14	ADK02770	67.8	30	14	ADK02770	Adk02770 Human 5-H
31	2	AAV80316	67.8	31	2	AAV80316	Aav80316 Reverse p
31	4	AAF89722	67.8	31	4	AAF89722	Aaf89722 PCR prime
33	6	ABA05757	67.8	33	6	ABA05757	Aba05757 Human NTF
34	8	ABZ59225	67.8	34	8	ABZ59225	Abz59225 Gentamic
36	14	ADY01040	67.8	36	14	ADY01040	Ady01040 PCR prime

	C	93	12.2	67.8	37	5	ABI97793	Abi97793	Non-endog
	94	95	12.2	67.8	37	5	ABI97794	Abi97794	Non-endog
			12.2	67.8	37	5	AAQ12334	Aaq12334	HPV exon-
			12.2	67.8	41	6	ABA05759	Human NTF	
			12.2	67.8	41	6	ABA05760	Human NTF	
			12.2	67.8	41	6	ABZ43055	Human ALD	
			12.2	67.8	41	6	ABZ46525	Human ALD	
			12.2	67.8	42	10	ABX93701	Abx93701	2C-methyl
			12.2	67.8	42	10	ABX93701	Abx93701	2C-methyl

## ALIGNMENTS

[illegible]

XX	WO200152902-A1.	
PN		
XX		
XX	26-JUL-2001.	
XX		
XX	15-JAN-2001; 2001WO-US001381.	
PF		
XX	24-JAN-2000; 2000US-00490208.	
XX		
XX	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett CF, Dean NM, Cowseert LM;	
XX		
DR	WPI; 2001-465340/50.	
XX		
PT	New antisense oligonucleotides for modulating the expression of inducible	
PT	nitric oxide synthase in cells or tissues, particularly useful for	
PT	treating e.g. immunological, cardiovascular or neurological disorders, or	
PT	ischemia.	
XX		
PS	Example 15; Page 83; 144pp; English.	

The invention relates to antisenese compounds, especially oligonucleotides, which are targeted to a nucleic acid encoding inducible nitric oxide synthase and which specifically hybridize to and modulate expression of inducible nitric oxide synthase. The antisenese compounds have immunomodulator, antidiabetic, cardiovascular, cardiac, neuroprotective, disorder and vasotonic activity. The antisenese oligonucleotides are useful for inhibiting the expression of inducible nitric oxide synthase in cells or tissues. In particular, the antisenese oligonucleotides are useful for treating diseases or disorders associated with inducible nitric oxide synthase, e.g. diabetes, immunological disorder, cardiovascular disorder, neurological disorder or ischaemia/reperfusion injury. The antisenese oligonucleotides are also useful for research and diagnostics. The present sequences that of an

CC antisense 2',O-methoxyethyl gapper oligonucleotide with a  
CC phosphorothioate backbone, a central "gap" region of ten nucleotides  
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine  
CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human  
CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)  
XX  
SQ Sequence 18 BP; 3 A; 3 C; 3 G; 9 T; 0 U; 0 Other;

Query Match	100.0%;	Score 18;	DB 4;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 17;		

Qy 1 TGTCACTTATCTGGATT 18  
|||  
db 1 TGTCACTTATCTGGATT 18

RESULT 2  
ADQ62106/c  
ID ADQ62106 standard; RNA; 19 BP.  
XX  
XX  
ADQ62106;  
XX  
09-SEP-2004 (first entry)  
XX  
DT  
DT  
XX  
XX  
XX  
DE Anti-NOS2A siRNA SEQ ID NO:1808.

XX Anastasia K, Angela R, Devin L, William M, Stephen S;  
PI  
XX WPI; 2004-420527/39.  
DR

Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases  
PT PT  
by selecting a target gene and measuring the functionality of the  
PT PT  
nucleotide sequences that are complementary to a stretch of nucleotides  
PT PT  
of the target sequence.

PS Example 12; SEQ ID NO 1808; 199pp; English.

The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of sequences of 19-25 nucleotides in length that are substantially complementary to a stretch of nucleotides of the target sequence, where the functionality is dependent upon non-target specific criteria. Also claimed are methods for gene-silencing, developing an siRNA algorithm for selecting siRNA, selecting an siRNA with improved functionality, selecting hyperfunctional siRNA, an siRNA molecule effective at silencing Bcl-2, and a kit for gene silencing comprising the siRNA. The siRNA molecule comprises a sequence substantially similar to a sequence consisting of GGAGAGUAGUGAUGAAGUA; GAAGUACUCCAUUUAAG; GUACGACCGCGGAUA; AGAUGAGUAGUGAUGAUC; GAAGACUGGACGAGUUA; UGCGGCGCCUUGUUGUAU; GAGAUAGUGAUGAAGUA; CC GGAGUAGUGAUGAAGUAC; and GAAGACUCUGCUCACUUG. The siRNA molecule comprises a sense strand and an anti-sense strand. The siRNA molecule comprises a hairpin. The siRNA molecule comprises between 18 and 30 base pairs. The kit comprises at least two siRNA, comprising a first optimised siRNA and a second optimised siRNA. The method is useful in selecting

CC siRNA for generating a gene silencing reagent. The present sequence is  
CC used in the exemplification of the invention.

XX SQ Sequence 19 BP; 8 A; 3 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 77.8%; Score 14; DB 12; Length 19;

XX Best Local Similarity 100.0%; Pred. NO. 2.1e+03; Indels 0; Gaps 0;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTCACCTTATCTGG 14

DB 14 TGTCACCTTATCTGG 1

RESULT 3

ADRI6179

ID ADRI6179 standard; DNA; 30 BP.

XX AC

ADRI6179;

XX DT

21-OCT-2004 (first entry)

XX DE

Yersinia pestis His-tagged-YscF amplifying PCR primer, HT-YscF Start.

XX KW

Immunogenic; medicament; antibacterial; vaccine; YscF; PCR; primer; ss.

XX OS

Yersinia pestis.

XX PN

US2004151727-A1.

XX PD

05-AUG-2004.

XX PF

18-JUL-2003; 2003US-00622220.

XX PR

31-JAN-2003; 2003US-0444076P.

XX PA

(NILL/) NILLES M L.

XX PI

(MAYS/) MATSON J S.

XX PI

Nilles ML, Matson JS;

XX DR

WPI; 2004-570705/55.

XX PT

New immunogenic composition comprises a recombinant YscF protein, useful as a vaccine for providing protection against a pathogen of Yersinia origin or for treating an animal infected with a Yersinia pathogen.

XX PS

Example 1; SEQ ID NO 15; 31pp; English.

XX CC

The present invention provides an immunogenic composition for providing protection to an animal against a pathogen of Yersinia origin. The invention is useful for the manufacture of a medicament for the treatment of a mammal infected with a Yersinia pathogen. The invention acts as an antibacterial and useful for the preparation of a vaccine against a pathogen of Yersinia origin. The present sequence is Yersinia pestis His-tagged (HT)-YscF DNA amplifying PCR primer. This sequence is used in the exemplification of the invention.

XX SQ

Sequence 30 BP; 6 A; 7 C; 7 G; 10 T; 0 U; 0 Other;

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 13; Length 30;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GTCACTTATCTGGATT 18

DB 14 GTCACTTATCTGGATT 30

RESULT 4

ADP13976

ID ADP13976 standard; DNA; 25 BP.

XX

AC ADP13976;

XX 26-AUG-2004 (first entry)

XX DE

Renal cell carcinoma differentially expressed gene probe #381.

XX KW

ss; diagnosis; non-blood disease; solid tumor; gene expression;

XX KW

peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

XX KW

head/neck cancer; differential expression; probe.

XX OS

Homo sapiens.

XX PN

WO2004048933-A2.

XX PD

10-JUN-2004.

XX PF

21-NOV-2003; 2003WO-US037481.

XX PR

21-NOV-2002; 2002US-0427982P.

XX PR

03-APR-2003; 2003US-0459782P.

XX PA

(AMHP ) WYETH.

XX PA

(TWIN/) TWINE N C.

XX PA

(BURC/) BURCZYNSKI M E.

XX PA

(TRBP/) TREPICCHIO W L.

XX PA

(DORN/) DORNER A.

XX PA

(STOV/) STOVER J A.

XX PA

(SLON/) SLONI D K.

XX PI

Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;

XX PI

Sloni DK;

XX DR

WPI; 2004-460799/43.

XX PT

Diagnosing non-blood disease such as solid tumor, involves comparing

XX PT

differential expression profile of specific genes in peripheral blood

XX PS

sample of subject with reference expression profile of specific genes.

XX PS

Disclosure; SEQ ID NO 712; 350pp; English.

XX CC

The invention relate to a method of diagnosing (M1) non-blood disease

XX CC

such as solid tumor by providing peripheral blood sample of human having

XX CC

non-blood disease, and comparing an expression profile of specific genes

XX CC

in the peripheral blood sample to reference expression profile of the

XX CC

genes, where each of the genes is differentially expressed in peripheral

XX CC

blood mononuclear cells (PBMCs) of patients having the disease as

XX CC

compared to PBMCs of normal humans. The method is useful for diagnosing

XX CC

non-blood disease such as solid tumor. The solid tumor is chosen from

XX CC

renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The

XX CC

peripheral blood sample comprises enriched PBMCs. The peripheral blood

XX CC

sample is a whole blood sample (claimed). (M1) is useful for identifying

XX CC

genes that are differentially expressed in peripheral blood samples

XX CC

isolated at different stages of progression, development or treatment of

XX CC

RCC and/or other solid tumors. This sequence corresponds to a probe to

XX CC

detect a gene that is differentially expressed and detected by the method

XX CC

of the invention.

XX SQ

Sequence 25 BP; 4 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match

Best Local Similarity 74.4%; Score 13.4; DB 12; Length 25;

XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CACTTATCTGGATT 18

DB 11 CACTGATCTGGATT 25

RESULT 5

ADP13977

ID ADP13977 standard; DNA; 25 BP.

XX AC

ADP13977;

```

XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #382.
XX DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
XX KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PA (AMHP ) WYETH.
XX PA (TWIN/) TWINE N C.
XX PA (BURC/) BURCZYNSKI M E.
XX PA (TREP/) TREPICCHIO W L.
XX PA (DORN/) DORNER A.
XX PA (STOV/) STOVER J A.
XX PA (SLOW/) SLOWI D K.
XX PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX PI Sloni DK;
XX DR WPI; 2004-460799/43.
XX PT Diagnosing non-blood disease such as solid tumor, involves comparing
XX PT differential expression profile of specific genes in peripheral blood
XX PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 713; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
XX CC such as solid tumor by providing peripheral blood sample of human having
XX CC non-blood disease, and comparing an expression profile of specific genes
XX CC in the peripheral blood sample to reference expression profile of the
XX CC genes, where each of the genes is differentially expressed in peripheral
XX CC blood mononuclear cells (PBMCs) of patients having the disease as
XX CC compared to PBMCs of normal humans. The method is useful for diagnosing
XX CC non-blood disease such as solid tumor. The solid tumor is chosen from
XX CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX CC sample is a whole blood sample (claimed). (M1) is useful for identifying
XX CC genes that are differentially expressed in peripheral blood samples
XX CC isolated at different stages of progression, development or treatment of
XX CC RCC and/or other solid tumors. This sequence corresponds to a probe to
XX CC detect a gene that is differentially expressed and detected by the method
XX CC of the invention.
XX SQ Sequence 25 BP; 8 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTATCTCGATT 18
Db 3 CACTGATCTGATT 17

RESULT 6
ADL01630
ID ADL01630 standard; DNA; 41 BP.
XX AC ADL01630;
XX
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DT 06-MAY-2004 (first entry)
XX Escherichia coli ydbB PCR primer #3.
XX DE protein co-ordinate data; protein co-ordinate data; ComA; crystal; ydbB;
XX KW PCR; primer; ss.
XX OS Escherichia coli.
XX PN WO2003050239-A2.
XX PD 19-JUN-2003.
XX PF 08-NOV-2002; 2002WO-US036087.
XX PR 09-NOV-2001; 2001US-0337683P.
XX PA (STRU-) STRUCTURAL GENOMIX INC.
XX PI Louie GV, Gajiwala KS, Buchanan SG;
XX DR WPI; 2003-532899/50.
XX PT Producing a computer-readable database comprising three-dimensional
XX PT molecular structural coordinates comprising obtaining three-dimensional
XX PT structural coordinates defining the protein or a binding pocket of the
XX PT protein.
XX PS Example 1; Page 65; 586pp; English.
XX CC The present invention relates to E. coli ComA protein (ADL01638) and its
XX CC protein co-ordinate data. The ComA crystalline protein is a heavy-atom
XX CC derivative crystal. The invention is useful for producing a computer-
XX CC readable database for solving the crystal and solution structures of
XX CC related and unrelated proteins, for screening, identifying and/or
XX CC designing protein analogs and modified proteins or compounds that bind
XX CC and/or modulate a biological activity of ComA or ydbB (ADL01633),
XX CC including inhibitors or activators of ComA or ydbB activity. PCR primers
XX CC ADL01630 and ADL01631 were used to amplify the coding sequence for ydbB
XX CC from E. coli genomic DNA. The PCR product was then ligated with T4 DNA
XX CC ligase into pSB3. The vector pSB3 is a modified version of pET26b wherein
XX CC the sequence of ADL01632 has been inserted into the NdeI site. The
XX CC resulting sequence of the gene after being ligated into the vector, from
XX CC the Shine-Dalgarno sequence through the stop site and the "original"
XX CC BamHI site is given in ADL01629.
XX SQ Sequence 41 BP; 13 A; 9 C; 5 G; 14 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 10; Length 41;
Best Local Similarity 93.3%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGA 15
Db 13 TGTCACCTTATCTGGA 27

RESULT 7
ABN39325
ID ABN39325 standard; DNA; 60 BP.
XX AC ABN39325;
XX DT 15-JUL-2002 (first entry)
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:12073.
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX KW splice variant; transcriptome; oligonucleotide library; ss.
XX OS Homo sapiens.
XX PN WO200210449-A2.
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XX PS Example 3; Page 11; 22pp; German.
XX CC This invention describes a novel method for the specific detection and
XX CC identification of retroviral nucleic acid (or retroviruses) comprising
XX CC isolation of DNA and/or RNA, subjecting this to reverse transcription-
XX CC polymerase chain reaction (RT-PCR) with one of two specified primer pairs
XX CC (or both pairs), purifying the amplicons and analyzing them by reverse
XX CC dot blot hybridization (RDBH) using immobilized, synthetic
XX CC oligonucleotide probes. The method is used to detect retroviruses (or
XX CC their nucleic acid) in cell cultures (or supernatants); body samples or
XX CC other biological materials. It produces an expression pattern of all
XX CC retroviruses in a single experiment, particularly for large scale surveys
XX CC to determine any correlations between diseases and activity of selected
XX CC retroviruses. If such a correlation is found, the method will allow early
XX CC diagnosis, or assessment of risk. An efficient, reliable and rapid method
XX CC for detecting all presently known endogenous and exogenous retroviruses
XX CC of human or animal origin with very low detection limit. The
XX CC amplification primers are universal and inclusion of a clamp and
XX CC restriction enzyme recognition site in them (i) improves primer/matrix
XX CC binding kinetics and allows amplification of Krise templates even if
XX CC there is not an exact match and (ii) facilitates subsequent cloning.
XX CC Using probes that do not overlap with primers overcomes the problem of
XX CC amplicons reacting, to some extent, with all probes in the array
XX SQ Sequence 45 BP; 11 A; 5 C; 10 G; 19 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 45;
Best Local Similarity 83.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
   |||||
Db 3 TATCAGTTATCTGGCTT 20

RESULT 10
ABSS5303
ID ABS55303 standard; DNA; 48 BP.
AC ABS55303;
XX 12-DEC-2002 (first entry)
DT PLAC promoter 5' PCR primer.
DE
XX Plasmid; transposon; selectable marker; transposase; promoter;
KW environmentally sensitive; bacterial; origin of replication; viability;
KW bacterial cell; Gram-negative; large-scale screening; gene multiplicity;
KW footprinting plasmid; PCR; primer; ss; PLAC.
XX Synthetic.
OS
XX US2002119573-A1.
XX 29-AUG-2002.
XX 28-FEB-2001; 2001US-00796088.
XX 28-FEB-2001; 2001US-00796088.
XX (SHAW/) SHAW K J.
XX (KENN/) KENNEY T.
XX (SHIM/) SHIMER G H.
XX Shaw KJ, Kenney T, Shimer GH;
XX WPI; 2002-740187/80.
XX Novel plasmid for determining importance of gene in viability of
XX organism, has transposon having marker gene, gene encoding transposase
XX linked to promoter, and environmentally sensitive bacterial origin of
XX replication.
XX Example 1; Page 4; 19pp; English.
XX The present invention relates to a new plasmid comprising a transposon
XX carrying a selectable marker gene, a gene encoding a transposase that
XX catalyses insertion of the transposon into genomic DNA in vivo, where the
XX gene is operably linked to a regulatable promoter, and an environmentally
XX sensitive bacterial origin of replication. The invention is useful for
XX determining if a bacterial gene of interest is important for viability of
XX bacterial cell (Gram-negative) from which it is derived. The invention is
XX also useful for large-scale screening of the multiplicity of genes. The
XX invention allows rapid and efficient determination of the role in cell
XX viability of a large number of genes. The present nucleic acid sequence
XX represents a PCR primer that was used in the invention for construction
XX of footprinting plasmids
XX SQ Sequence 48 BP; 13 A; 11 C; 6 G; 18 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 48;
Best Local Similarity 83.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
   |||||
Db 16 TGTCACTTACCTGGAAT 33

RESULT 11
ABSS5302/c
ID ABS55302 standard; DNA; 48 BP.
XX
AC ABS55302;
XX 12-DEC-2002 (first entry)
DT Chloramphenicol (cat) gene 3' PCR primer.
DE
XX Plasmid; transposon; selectable marker; transposase; promoter;
KW environmentally sensitive; bacterial; origin of replication; viability;
KW bacterial cell; Gram-negative; large-scale screening; gene multiplicity;
KW footprinting plasmid; PCR; primer; ss; chloramphenicol; cat.
XX Unidentified.
OS
XX US2002119573-A1.
XX 29-AUG-2002.
XX 28-FEB-2001; 2001US-00796088.
XX 28-FEB-2001; 2001US-00796088.
XX (SHAW/) SHAW K J.
XX (KENN/) KENNEY T.
XX (SHIM/) SHIMER G H.
XX Shaw KJ, Kenney T, Shimer GH;
XX WPI; 2002-740187/80.
XX Novel plasmid for determining importance of gene in viability of
XX organism, has transposon having marker gene, gene encoding transposase
XX linked to promoter, and environmentally sensitive bacterial origin of
XX replication.
XX Example 1; Page 4; 19pp; English.
XX The present invention relates to a new plasmid comprising a transposon
XX carrying a selectable marker gene, a gene encoding a transposase that
XX catalyses insertion of the transposon into genomic DNA in vivo, where the
XX gene is operably linked to a regulatable promoter, and an environmentally
XX sensitive bacterial origin of replication. The invention is useful for
XX determining if a bacterial gene of interest is important for viability of

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CC bacterial cell (Gram-negative) from which it is derived. The invention is  
 CC also useful for large-scale screening of the multiplicity of genes. The  
 CC invention allows rapid and efficient determination of the role in cell  
 CC viability of a large number of genes. The present nucleic acid sequence  
 CC represents a PCR primer that was used in the invention for construction  
 CC of footprinting plasmids

XX Sequence 48 BP; 18 A; 6 C; 11 G; 13 T; 0 U; 0 Other;  
 SQ Query Match 73.3%; Score 13.2; DB 6; Length 48;  
 Best Local Similarity 83.3%; Pred. No. 6e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18  
 |||||  
 DB 33 TGTCACTTAACCTGGAAT 16

RESULT 12  
 ABN52886  
 ID ABN52886 standard; DNA; 65 BP.  
 XX AC  
 XX ABN52886;  
 DT 15-JUL-2002 (first entry)  
 XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25634.  
 XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX OS Mus musculus.

XX WO200210449-A2.  
 XX 07-FEB-2002.  
 XX 20-JUL-2001; 2001WO-IB001903.  
 XX 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX WPI; 2002-257383/30.  
 XX New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.

XX Example 1; SEQ ID NO 25634; 47pp; English.  
 XX The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular

CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 65 BP; 14 A; 14 C; 19 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 73.3%; Score 13.2; DB 6; Length 65;  
 Best Local Similarity 83.3%; Pred. No. 6.2e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18  
 |||||  
 DB 32 TGTCACTATCTGGATAT 49

RESULT 13  
 ADP80938/c  
 ID ADP80938 standard; cDNA; 75 BP.  
 XX AC  
 XX ADP80938;  
 DT 09-SEP-2004 (first entry)  
 XX DE Mouse DnaJ homologue subfamily A member 2 nucleotide SEQ ID NO:163.  
 XX KW c-fos; c-fos interacting protein; fos interacting protein chromosome X;  
 KW Fip-cx; screening; Fc-fos interacting protein inhibitor; mouse;  
 KW DnaJ homologue subfamily A member 2; gene; ss.

XX Mus musculus.  
 XX Key Location/Qualifiers  
 FH 1..75  
 CDS /tag= a  
 FT /product= "DnaJ homologue subfamily A member 2"  
 FT WO2004053121-A1.  
 XX 24-JUN-2004.

XX 19-NOV-2003; 2003WO-JP014749.  
 XX 11-DEC-2002; 2002JP-00360046.  
 XX (UYKE-) UNIV KEIO.

XX Miyamoto E, Ishizaka M, Yanagawa H;  
 XX WPI; 2004-517250/49.  
 DR P-PSDB; ADP80874.

XX New proteins that interact with fos, e.g., fos interacting protein  
 PT chromosome X (Fip-cx).  
 XX Claim 107; SEQ ID NO 163; 192pp; Japanese.

XX The present invention describes a protein (I) that interacts with c-fos  
 CC (e.g., fos interacting protein chromosome X (Fip-cx), Fip-cx.1, fos  
 CC interacting protein chromosome ex.2, or fos interacting protein  
 CC chromosome 4). Also described: (1) a nucleic acid (II) that encodes (I);  
 CC (2) an inhibitor (III) that inhibits the interaction of (I) encoded by  
 CC (II) with c-fos protein; (3) an inhibitor (IV) that inhibits interaction  
 CC of a protein with c-fos protein; and (4) detecting (M1) the interaction  
 CC of a protein as mentioned in (3) with c-fos protein, by contacting the  
 CC protein with c-fos, to form a complex. (I) is useful for detecting its  
 CC interaction with c-fos, to form a complex. (M1) is useful for screening  
 CC the protein that interacts with c-fos which involves performing the  
 CC detection process and selecting the protein that interacts with c-fos.  
 CC (M1) is useful for screening a protein that interacts with c-fos which  
 CC involves performing (M1) and selecting the detected protein. (I) is  
 CC useful for screening inhibitors that interact with c-fos. The present

CC sequence encodes a mouse DnaJ homologue subfamily A member 2 amino acid  
CC sequence, which can interact with c-fos in the exemplification of the  
CC present invention.

XX SQ Sequence 75 BP; 25 A; 13 C; 27 G; 10 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 12; Length 75;  
Best Local Similarity 83.3%; Pred. No. 6.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATTT 18  
| | | | | | | | | |  
Db 23 TCTCGCTCTCTGGATTT 6

RESULT 14  
ADU73604  
ID ADU73604 standard; DNA; 20 BP.

XX AC ADU73604;

XX DT 10-FEB-2005 (first entry)

XX DE Probe N-STX1-F2 for amplified shiga-like toxin stx1 gene detection.

XX KW Analyte detection; Nucleic acid detection; chromatography;

XX KW shiga-like toxin I; probe; ss.

XX OS Escherichia coli.

XX FH Key Location/Qualifiers

FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 5' Amine"

XX WO2004099438-A1.

XX PD 18-NOV-2004.

XX PF 30-APR-2004; 2004WO-BE000061.

XX PR 07-MAY-2003; 2003US-0468805P.

XX PA (CORI-) CORIS BIOCONCEPT SPRL.

XX PI Renuart I, Mertens P, Leclipteux T;

XX DR WPI; 2004-821682/81.

XX PS New sheet-like chromatographic device comprising an application region, a  
XX detection region possibly with a control region and optionally an  
XX adsorbent region, useful in detecting or quantifying an analyte in a  
XX biological sample.

XX Example 2; SEQ ID NO 1; 36pp; English.

XX CC The invention relates to methods and devices for detecting analytes in a  
XX biological sample, preferably a clean liquid sample. Sheet-like  
XX oligochromatographic devices are provided, in particular dipsticks, flow-  
XX through and lateral flow devices, having an application region  
XX (optionally with conjugation pad), a detection region (possibly with  
XX control portion, e.g. control lines) and optionally an absorbent region.  
XX The detection region comprises at least one capture reagent specifically  
XX recognizing a hapten or peptide conjugated with or coupled to an analyte-  
XX specific oligonucleotide. The application region comprises at least one  
XX specific labeled conjugate (with direct or indirect label) preferably an  
XX oligonucleotide (DNA, RNA, PNA, LNA) that hybridizes specifically with  
XX the analyte and generally designated as a probe. The device allows the  
XX presence of a polynucleotide to be specifically detected directly or  
XX after molecular amplification steps. The device is easy to handle and  
XX allows rapid but accurate detection and/or diagnosis. The present  
XX sequence is that of oligonucleotide probe N-STX1-F2 for the Escherichia

CC coli strain O157:H7 shiga-like toxin I stx1 gene. The probe was used in  
CC an example from the invention in which an oligochromatographic dipstick  
CC was designed for the specific detection of amplified stx1 and stx2 genes.

XX SQ Sequence 20 BP; 4 A; 3 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTTATCTGGATTT 18  
| | | | | | | | | |  
Db 4 CTTATCTGGATTT 16

RESULT 15  
ADR70635  
ID ADR70635 standard; DNA; 50 BP.

XX AC ADR70635;

XX DT 21-OCT-2004 (first entry)

XX DE Exemplary set-unique oligonucleotide #4 for Escherichia coli Shiga gene.

XX KW unique genomic sequence; similarity search engine; genomic database;

XX KW BLAST search engine; GenBank; ss; Shiga gene.

XX OS Escherichia coli.

XX PN WO2004065565-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-US001701.

XX PR 23-JAN-2003; 2003US-0441745P.

XX PR 23-JAN-2003; 2003US-0441806P.

XX PA (SCIT-) SCI APPL INT CORP.

XX PI Eley DG, Vockley JG;

XX DR WPI; 2004-562161/54.

XX PS Identifying genomic and oligonucleotide sequences unique to a set of  
XX organisms, useful for gathering sequences on organisms present in a  
XX sample, comprises searching selected genomic database using the query and  
XX the similarity search engine.

XX PS Disclosure; Page 20; 34pp; English.

XX CC The specification describes a method for identifying genomic sequences  
XX and oligonucleotide sequences unique to a set of organisms. The method  
XX comprises obtaining genomic data characteristic of the set, formatting  
XX the genomic data into at least one query-length sequence, each query-  
XX length sequence being of a format compatible with a similarity search  
XX engine, searching a selected genomic database using the query and the  
XX similarity search engine, and parsing the results of the search for those  
XX sequences showing uniqueness to the set. The similarity search engine is  
XX a BLAST search engine. The selected database is GenBank. The method is  
XX useful for identifying genomic sequences and oligonucleotide sequences  
XX unique to a set of organisms. The method is also useful for gathering  
XX sequences on one or more sets of organisms present in a sample. ADR70632-  
XX ADR70641 represent exemplary set-unique oligonucleotides for Escherichia  
XX coli Shiga gene, identified using the method of the invention.

XX SQ Sequence 50 BP; 11 A; 10 C; 10 G; 19 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 13; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 6 CTTATCTGGATTT 18  
 DB 22 CTTATCTGGATTT 34

RESULT 16  
 AAA85172  
 ID AAA85172 standard; DNA; 19 BP.  
 AC AAA85172;  
 XX 04-DEC-2000 (first entry)  
 DT  
 DE Cyclin G1 ribozyme binding site #197.  
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 XX Mammalia.  
 OS  
 XX WO200032765-A2.  
 PN  
 XX 08-JUN-2000.  
 PD  
 XX 06-DEC-1999; 99WO-US028772.  
 PF  
 XX 04-DEC-1998; 98US-0110954P.  
 PR  
 XX (IMMU-) IMMUSOL INC.  
 PA  
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;  
 PI  
 XX WPI; 2000-412314/35.  
 DR  
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 PCNA and Cyclin B1.  
 PT  
 XX Disclosure; Page 88; 109pp; English.  
 PS  
 XX The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 CC  
 XX Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 71.1%; Score 12.8; DB 3; Length 19;  
 Best Local Similarity 87.5%; Pred. No. 9e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17  
 DB 4 GTCCCTTAACTGGATT 19

RESULT 17  
 AAA85173  
 ID AAA85173 standard; DNA; 19 BP.  
 AC AAA85173;  
 XX 04-DEC-2000 (first entry)  
 DT  
 DE Cyclin G1 ribozyme binding site #198.  
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 XX Mammalia.  
 OS  
 XX WO200032765-A2.  
 PN  
 XX 08-JUN-2000.  
 PD  
 XX 06-DEC-1999; 99WO-US028772.  
 PF  
 XX 04-DEC-1998; 98US-0110954P.  
 PR  
 XX (IMMU-) IMMUSOL INC.  
 PA  
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;  
 PI  
 XX WPI; 2000-412314/35.  
 DR  
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 PCNA and Cyclin B1.  
 PT  
 XX Disclosure; Page 88; 109pp; English.  
 PS  
 XX The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 CC  
 XX Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 71.1%; Score 12.8; DB 3; Length 19;  
 Best Local Similarity 87.5%; Pred. No. 9e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17  
 DB 4 GTCCCTTAACTGGATT 19

RESULT 18  
 AAA60334  
 ID AAA60334 standard; DNA; 19 BP.  
 AC AAA60334;  
 XX 10-SEP-2001 (first entry)  
 DT  
 DE Cyclin G1 ribozyme binding site SEQ ID NO:2758.  
 DE  
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
 KW recognition site; target; ribozyme binding site; eye disease; vulvetry;  
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytotstatic;  
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;  
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
 KW sickle cell retinopathy; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 XX  
 XX WO200130362-A2.  
 PN  
 XX 03-MAY-2001.  
 PD  
 XX 26-OCT-2000; 2000WO-US029500.  
 PF  
 XX 26-OCT-1999; 99US-0161532P.  
 PR  
 XX (IMMU-) IMMUSOL INC.  
 PA

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XX Robbins JM, Tritz R;
PI WPI; 2001-300427/31.
DR
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 272; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 71.1%; Score 12.8; DB 5; Length 19;
Best Local Similarity 87.5%; Pred. No. 9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17
Db 4 GTCCCTTAACCTGGATT 19

RESULT 19
AAH60335
ID AAH60335 standard; DNA; 19 BP.
XX
AC AAH60335;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cyclin G1 ribozyme binding site SEQ ID NO:2759.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
XX
XX
XX (IMMU-) IMMUSOL INC.
XX Robbins JM, Tritz R;
PI WPI; 2001-300427/31.
DR
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 272; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 71.1%; Score 12.8; DB 5; Length 19;
Best Local Similarity 87.5%; Pred. No. 9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17
Db 3 GTCCCTTAACCTGGATT 18

RESULT 20
AAH82405/c
ID AAF82405 standard; DNA; 23 BP.
XX
AC AAF82405;
XX
DT 26-JUN-2001 (first entry)
XX
DE Mealworm encapsulation protein DNA probe #2.
DE
KW Mealworm; encapsulation; immunostimulant; probe; ss.
XX
OS Tenebrio molitor.
XX
XX Key Location/Qualifiers
FH modified_base 6 /*tag= a
FT /mod_base= i
FT modified_base 12 /*tag= b
FT /mod_base= i
XX
XX JP2001037488-A.
XX
XX 13-FEB-2001.
XX
XX 29-NOV-1999; 99JP-00338594.
XX
XX 07-JUL-1999; 99KR-00027933.
XX

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PR 26-JUL-1999; 99KR-00031172.  
PA (SAMY-) SAMYANG GENEX CORP.  
XX  
DR WPI; 2001-285602/30.  
PT Novel protein involved in encapsulation, used as an immunological  
PT activity enhancer.  
XX  
PS Example 4; Page 6; 23pp; Japanese.  
XX  
CC The present probe is provided in a specification relating a mealworm  
CC protein that participates in encapsulation, which is a cellular defensive  
CC reaction. The invention provides an encapsulation polypeptide comprising  
CC residues 1-754 or 18-754 of a 754 amino acid sequence, or 1-579 or 16-579  
CC of a 579 amino acid sequence, both fully defined in the specification, or  
CC a mutant having a replacement, deletion or insertion of an amino acid in  
CC at least one residue of the sequence. The protein can be used as an  
CC immunological activity enhancer  
XX  
SQ Sequence 23 BP; 9 A; 3 C; 2 G; 2 T; 0 U; 7 Other;  
Query Match 71.1%; Score 12.8; DB 4; Length 23;  
Best Local Similarity 61.1%; Pred. No. 9.2e+03;  
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
OY 1 TGTCACCTATCTGGATT 18  
Db 19 TTTCTTATTTGTTGTT 2  
RESULT 21  
AAD26335  
ID AAD26335 standard; DNA; 24 BP.  
XX  
AC AAD26335;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human beta-tubulin gene exon 1 sequencing SE1 reverse PCR primer.  
XX  
KW Human; beta-tubulin; GTP-binding site; prognosis; lung cancer;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200190413-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 17-MAY-2001; 2001WO-US016004.  
XX  
PR 19-MAY-2000; 2000US-00574788.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Rosell R, Monzo M;  
XX  
WPI; 2002-097668/13.  
XX  
PT Prognosticating efficacy of anticancer agents in a patient suffering from  
PT cancer involves analyzing sample from patient for presence of mutation in  
PT GTP-binding site or carboxy-terminal region of exon 4 of tubulin gene.  
XX  
PS Example 7; Page 22; 26pp; English.  
XX  
CC The invention relates to a method for prognosticating efficacy of  
CC anticancer agent in a patient suffering from cancer. The method involves  
CC analysing a biological sample from a patient for the presence of mutation  
CC in the GTP-binding site or carboxy-terminal region of exon 4 of mutant  
CC tubulin genes. The method is useful for prognosticating the efficacy of  
CC anticancer agents (an anti-tubulin agent) in patients suffering from lung  
CC cancer. The present sequence is a PCR primer used for sequencing human

CC beta-tubulin gene exon 1  
XX  
SQ Sequence 24 BP; 5 A; 4 C; 2 G; 13 T; 0 U; 0 Other;  
Query Match 71.1%; Score 12.8; DB 6; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 3 TCACCTTATCTGGATT 18  
Db 7 TAACTTACCTGGATT 22  
RESULT 22  
AAS13868/c  
ID AAS13868 standard; DNA; 27 BP.  
XX  
AC AAS13868;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Tn5-based transposon PCR primer Tn7L.PCR.  
XX  
KW Transposon Tn5; sequencing primer; transposon-disrupted gene;  
KW Gene function; ss.  
XX  
OS Synthetic.  
XX  
PN WO200171040-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US009003.  
XX  
PR 23-MAR-2000; 2000US-0191561P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Sharpe PL, Cheng Q, Nagarajan V;  
XX  
WPI; 2001-611517/70.  
XX  
PT Identifying essential genes responsible for specific phenotypes in  
PT microorganisms by inserting a transposon-disrupted gene homolog into the  
PT microorganism genome is useful to determine gene function.  
XX  
PS Example 6; Page 28; 51pp; English.  
XX  
CC The invention relates to a method of identifying an essential gene  
CC responsible for a specific phenotype in a recombination proficient  
CC microorganism. The method comprises inserting a transposon-disrupted gene  
CC homologue into the microorganism genome and selecting for transformants  
CC having a changed phenotype. The method is used to elucidate the function  
CC of known gene sequences and can be used on microorganisms which are not  
CC naturally transformable. The present sequence represents Tn5-based  
CC transposon sequencing primer Tn7L.PCR, used in the method of the  
XX invention  
XX  
SQ Sequence 27 BP; 10 A; 7 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 71.1%; Score 12.8; DB 4; Length 27;  
Best Local Similarity 87.5%; Pred. No. 9.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 TGTCACTTATCTGGAT 16  
Db 18 TTTCACCTTATCTGGTT 3  
RESULT 23  
ABZ48041/c  
ID ABZ48041 standard; DNA; 41 BP.  
XX

AC ABZ48041;  
XX 26-JUN-2003 (first entry)  
XX Human ATP-binding cassette ABCG5 gene polymorphic site, #4824.  
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
KW drug evaluation; drug screening; genotyping; genetic profiling;  
KW therapeutic customisation; adverse reaction; clinical trial;  
KW drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(12,A)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
FT replace(21,A)  
FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
XX WO200252044-A2.  
XX  
XX 04-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-JP011592.  
XX  
XX 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE ) RIKEN KK.  
XX  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.  
XX  
XX Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.  
XX  
XX Claim 23; Page 156; 2785pp; English.  
XX  
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to a an increase in the range of

CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 13 A; 9 C; 10 G; 9 T; 0 U; 0 Other;  
Query Match 71.1%; Score 12.8; DB 6; Length 41;  
Best Local Similarity 87.5%; Pred. No. 9.6e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 TCACCTATCTGGATT 18  
Db 32 TTACTTATCAGGATT 17  
RESULT 24  
ABZ48040/c  
ID ABZ48040 standard; DNA; 41 BP.  
XX  
XX AC ABZ48040;  
XX  
XX 26-JUN-2003 (first entry)  
XX  
XX Human ATP-binding cassette ABCG5 gene polymorphic site, #4823.  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
KW drug evaluation; drug screening; genotyping; genetic profiling;  
KW therapeutic customisation; adverse reaction; clinical trial;  
KW drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
XX OS Homo sapiens.  
XX  
XX FH Key Location/Qualifiers  
FT variation replace(21,A)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
FT variation replace(30,A)  
FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
XX WO200252044-A2.  
XX  
XX 04-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-JP011592.  
XX  
XX 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE ) RIKEN KK.  
XX  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.  
XX  
XX Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.  
XX  
XX Claim 23; Page 156; 2785pp; English.  
XX  
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to a an increase in the range of

CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy

XX SQ Sequence 41 BP; 16 A; 10 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 6; Length 41;

Best Local Similarity 87.5%; Pred. No. 9.6e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18

DB 41 TTACTTATCAGGATT 26

# RESULT 25

AAZ68526/c

ID AAZ68526 standard; DNA; 47 BP.

AC AAZ68526;

XX 10-SEP-2001 (first entry)

XX Human map-related biallelic marker SEQ ID NO:2874.

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation; diagnosis;

XX single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

XX variation replace(24,C)

FT /\*tag= a

FT /standard\_name= "single nucleotide polymorphism"

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB0000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST ) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.

PS Claim 3; Page 843; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention

XX SQ Sequence 47 BP; 15 A; 7 C; 7 G; 18 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 3; Length 47;

Best Local Similarity 87.5%; Pred. No. 9.8e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGAT 16

DB 22 TATCCTTATCTGAAT 7

Search completed: March 3, 2006, 08:00:39

Job time : 123.534 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds  
(without alignments)  
1353.240 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18  
Sequence: 1 tgcacttatctggattt 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*  
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4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/6H COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/6TUS COMB.seq.\*  
7: /cgn2\_6/prodata/1/ina/6TUS COMB.seq.\*  
8: /cgn2\_6/prodata/1/ina/6TUS COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/6TUS COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 1	13.4	74.4	25	3	US-09-396-196G-102305
C 2	13.2	73.3	25	3	US-09-396-196G-61721
C 3	13.2	73.3	25	3	US-09-396-196G-111634
C 4	12.8	71.1	19	3	US-09-696-791-2758
C 5	12.8	71.1	19	3	US-09-696-791-2759
C 6	12.8	71.1	27	3	US-09-808-658-7
C 7	12.8	71.1	47	3	US-09-422-978-2874
C 8	12.8	71.1	50	3	US-10-131-827-3958
C 9	12.8	71.1	51	3	US-09-693-146-15
C 10	12.8	71.1	54	3	US-09-693-146-17
C 11	12.4	68.9	15	3	US-09-142-913-26
C 12	12.4	68.9	15	9	5182195-46
C 13	12.4	68.9	25	3	US-09-396-196G-93855
C 14	12.4	68.9	42	2	US-08-790-963-17
C 15	12.4	68.9	42	3	US-09-371-774-17
C 16	12.4	68.9	42	3	US-09-875-082-17
C 17	12.4	68.9	47	3	US-09-422-978-1643
C 18	12.4	68.9	47	3	US-09-422-978-1659
C 19	12.4	68.9	63	3	US-09-513-999C-15454
C 20	12.2	67.8	21	3	US-09-215-221-30
C 21	12.2	67.8	25	3	US-09-396-196G-117798
C 22	12.2	67.8	25	3	US-09-396-196G-117799
C 23	12.2	67.8	30	3	US-09-292-071-6
C 24	12.2	67.8	30	3	US-09-292-071-11
C 25	12.2	67.8	30	3	US-09-292-069A-6
C 26	12.2	67.8	30	3	US-09-292-069A-11
C 27	12.2	67.8	30	3	US-09-418-721-6
C 28	12.2	67.8	30	3	US-09-418-721-11
C 29	12.2	67.8	30	3	US-09-767-013-6
C 30	12.2	67.8	30	3	US-09-767-013-11
C 31	12.2	67.8	30	3	US-09-292-072-6
C 32	12.2	67.8	30	3	US-09-292-072-11
C 33	12.2	67.8	30	3	US-09-170-496D-120
C 34	12.2	67.8	30	3	US-09-170-496D-236
C 35	12.2	67.8	30	3	US-10-176-255-6
C 36	12.2	67.8	30	3	US-10-176-255-11
C 37	12.2	67.8	31	3	US-09-445-375A-20
C 38	12.2	67.8	37	3	US-09-826-509-245
C 39	12.2	67.8	37	3	US-09-826-509-246
C 40	12.2	67.8	50	2	US-08-171-389-543
C 41	12.2	67.8	50	2	US-08-123-936-543
C 42	12.2	67.8	50	2	US-08-475-228A-543
C 43	12.2	67.8	50	3	US-08-482-080A-543
C 44	12.2	67.8	50	3	US-09-354-947-543
C 45	12.2	67.8	50	3	US-09-993-346-543
C 46	12.2	67.8	50	3	US-10-131-827-74
C 47	12.2	67.8	50	6	PCT-US93-12388-543
C 48	12.2	67.8	53	3	US-08-956-171B-2066
C 49	12.2	67.8	53	3	US-08-781-986A-2066
C 50	12	66.7	25	3	US-09-396-196G-101308
C 51	12	66.7	25	3	US-09-396-196G-101319
C 52	12	66.7	25	3	US-09-396-196G-101320
C 53	12	66.7	25	3	US-09-396-196G-101321
C 54	11.8	65.6	25	2	US-08-474-542A-42
C 55	11.8	65.6	20	2	US-08-457-648-42
C 56	11.8	65.6	21	3	US-09-657-472-1870
C 57	11.8	65.6	25	3	US-09-396-196G-19519
C 58	11.8	65.6	25	3	US-09-396-196G-19520
C 59	11.8	65.6	25	3	US-09-396-196G-121239
C 60	11.8	65.6	32	2	US-08-222-616-39
C 61	11.8	65.6	32	3	US-08-446-648-39
C 62	11.8	65.6	32	6	PCT-US95-04228-39
C 63	11.8	65.6	34	2	US-08-468-352-56
C 64	11.8	65.6	30	3	US-10-131-827-1965
C 65	11.8	65.6	57	2	US-08-039-974B-31
C 66	11.6	64.4	18	3	US-10-014-012-58
C 67	11.6	64.4	22	3	US-08-983-605-190
C 68	11.6	64.4	24	2	US-08-632-575B-24
C 69	11.6	64.4	24	3	US-09-199-542B-24
C 70	11.6	64.4	25	3	US-09-396-196G-25786
C 71	11.6	64.4	25	3	US-09-396-196G-43129
C 72	11.6	64.4	25	3	US-09-396-196G-56053
C 73	11.6	64.4	25	3	US-09-396-196G-59217
C 74	11.6	64.4	25	3	US-09-396-196G-59217
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C 76	11.6	64.4	25	3	US-09-396-196G-67237
C 77	11.6	64.4	25	3	US-09-396-196G-78819
C 78	11.6	64.4	25	3	US-09-396-196G-121367
C 79	11.6	64.4	25	3	US-09-396-196G-121368
C 80	11.6	64.4	28	3	US-09-396-196G-123611
C 81	11.6	64.4	28	3	US-08-975-982-13
C 82	11.6	64.4	29	2	US-08-859-998-1359
C 83	11.6	64.4	29	3	US-09-225-928-1359
C 84	11.6	64.4	29	3	US-09-225-201B-1359
C 85	11.6	64.4	30	3	US-09-423-439-24
C 86	11.6	64.4	32	3	US-09-199-542B-74
C 87	11.6	64.4	39	3	US-10-211-948-6
C 88	11.6	64.4	47	3	US-09-422-978-481
C 89	11.6	64.4	49	2	US-08-392-771-3
C 90	11.6	64.4	50	2	US-08-860-882A-17
C 91	11.6	64.4	50	3	US-09-423-439-21
C 92	11.6	64.4	50	3	US-09-011-769A-13
C 93	11.6	64.4	50	3	US-10-131-827-1583
C 94	11.6	64.4	61	3	US-09-171-945-44
C 95	11.6	64.4	61	3	US-09-171-945-45
C 96	11.6	64.4	61	3	US-09-910-059-44
C 97	11.6	64.4	61	3	US-09-910-059-45





OTHER INFORMATION: Cyclin G1 ribozyme binding site  
US-09-696-791-2759

Query Match 71.1%; Score 12.8; DB 3; Length 47;  
Best Local Similarity 87.5%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels

Qy 1 TGTCACCTTATCTGGAT 16  
|||  
Dy 22 TATCACTTATCTGAAT 7

## RESULT 8

US-10-131-827-3958  
; Sequence 3958, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:

APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robe  
APPLICANT: Ly, Ngoc

APPLICANT: LY, NGOC  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR D  
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE OF INVENTION: CIRCUITS FOR ELECTRONIC  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: IIS/10/131-827

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; CURRENT AFFILIATION NUMBER: US/10/131,8
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10,005 280

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;  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ;  
 ; PRIOR FILING DATE: 2001-10-22  
 ;  
 ; PRIOR APPLICATION NUMBER: US 200,000,754

; PRIOR APPLICATION NUMBER: US 60/296,764  
 ;  
 ; PRIOR FILING DATE: 2001-06-08

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; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 39  
; LENGTH: 50

LENGTH: 30  
TYPE: DNA  
ORGANISM:

US-10-131-827-3958 .  
; ORGANISM: HOMO SAPIENS

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Query Match      71.1%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels
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Qy 2 GTCACTTATCTGGATT 17  
||| ||| ||| ||| |||  
Db 20 GTCTCTTGCTCTGGATT 35

RESULT. T 9

RESULT 9  
US-09-693-146-15/c  
; Sequence 15, Application US/09693146  
: Patent No. 6413758

APPLICANT: YU SHI

APPLICANT: Xu, Siuang-yong  
APPLICANT: Zhu, Zhenyu  
APPLICANT: Yang, Jia-jing

APPLICANT: Xiao, Jian-ping  
TITLE OF INVENTION: Method For Cloning And Expression Of Bpm1 Restriction  
TITLE OF INVENTION: Endonuclease In E. coli

;  
; TITLE OF INVENTION: Endonuclease In E. coli  
;  
; FILE REFERENCE: NEB-183

; CURRENT APPLICATION NUMBER: US/09/693,146  
 ; CURRENT FILING DATE: 2000-10-20

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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0

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; COLINFRE. INCREMENT VAR. 2...
; SEQ ID NO 15
; LENGTH. 51

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; LENGTH: 51
; TYPE: DNA
; ORGANISM: Drosophila melanogaster

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; ORGANISM: Bacillus pumilus  
US-09-693-146-15

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Query Match      71.1%; Score 12.8; DB 3; Length 51;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACTTATCTGGATTT 18
Db 35 TCACTTATATGCATTT 20

RESULT 10
US-09-693-146-17/c
; Sequence 17, Application US/09693146
; Patent No. 6413758
; GENERAL INFORMATION:
; APPLICANT: Xu, Shuang-yong
; APPLICANT: Zhu, Zhenyu
; APPLICANT: Xiao, Jian-ping
; TITLE OF INVENTION: Method For Cloning And Expression Of BpmI Restriction
; FILE REFERENCE: NEB-183
; CURRENT APPLICATION NUMBER: US/09/693,146
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Bacillus pumilus
US-09-693-146-17

Query Match      71.1%; Score 12.8; DB 3; Length 54;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACTTATCTGGATTT 18
Db 38 TCACTTATATGCATTT 23

RESULT 11
US-09-142-913-26
; Sequence 26, Application US/09142913A
; Patent No. 6573073
; GENERAL INFORMATION:
; APPLICANT: HARRIS, ANN
; TITLE OF INVENTION: CFTR GENE REGULATOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,913A
; FILING DATE: 18-Sep-1998
; CLASSIFICATION: <Unknown>
; 20-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB97/00787
; FILING DATE: <Unknown>
; APPLICATION NUMBER: GB 9605808.6
; FILING DATE: 20-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1283-37

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-142-913-26

Query Match      68.9%; Score 12.4; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
Db 1 TGTCACTTATCTTG 14

RESULT 12
5182195-46
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIHIKO;YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:46:
; LENGTH: 15
; 5182195-46

Query Match      68.9%; Score 12.4; DB 9; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
Db 1 TGTCACTTATCTTG 14

RESULT 13
US-09-396-196G-93855
; Sequence 93855, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-93855

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGA 15
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; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020Cp1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1643  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-5364-95 : polymorphic base C or T  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 47  
; OTHER INFORMATION: n=a, g, c or t  
US-09-422-978-1643

Query Match 68.9%; Score 12.4; DB 3; Length 47;

Best Local Similarity 81.2%; Pred. No. 3.4e+03; Length 47;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACCTATCTGGATT 18  
|||||:|||||  
Db 17 TCACCTATCTGGATT 32

RESULT 18

US-09-422-978-1659/c

; Sequence 1659, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020Cp1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1659  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-5438-70 : polymorphic base C or T  
US-09-422-978-1659

Query Match 68.9%; Score 12.4; DB 3; Length 47;

Best Local Similarity 81.2%; Pred. No. 3.4e+03; Length 47;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACCTATCTGGATT 18  
|||||:|||||  
Db 30 TCACCTATCTGGATT 15

RESULT 19

US-09-513-999C-15454/c

; Sequence 15454, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 15454  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-15454

Query Match 68.9%; Score 12.4; DB 3; Length 63;

Best Local Similarity 92.9%; Pred. No. 3.5e+03; Length 63;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTTATCTGGATT 18  
|||||:|||||  
Db 49 ACATATCTGGATT 36

RESULT 20

US-09-215-221-30/c

; Sequence 30, Application US/09215221  
; Patent No. 6265562  
; GENERAL INFORMATION:  
; APPLICANT: EILERS, MARTIN  
; APPLICANT: BUERGIN, ANDREA  
; APPLICANT: SEDLACEK, HANS-HARALD  
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY  
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF  
; FILE REFERENCE: 026083/0192  
; CURRENT APPLICATION NUMBER: US/09/215,221  
; CURRENT FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 197 56 975.7  
; PRIOR FILING DATE: 1997-12-20  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-215-221-30

Query Match 67.8%; Score 12.2; DB 3; Length 21;

Best Local Similarity 82.4%; Pred. No. 4e+03; Length 21;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCACCTATCTGGATT 18  
|||||:|||||  
Db 18 GACGCTTTCTGGATT 2

RESULT 21

US-09-396-196G-117798

; Sequence 117798, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 117798  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-09-396-196G-117798

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18  
 DB 9 GTCACTTATATGCGCTT 25

RESULT 22  
 US-09-396-196G-117799  
 ; Sequence 117799, Application US/09396196G  
 ; Patent No. 6821724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Wittmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/09/396,196G  
 ; CURRENT FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 117799  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-09-396-196G-117799

Query Match 67.8%; Score 12.2; DB 3; Length 25;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18  
 DB 3 GTCACTTATATGCGCTT 19

RESULT 23  
 US-09-292-071-6/c  
 ; Sequence 6, Application US/09292071  
 ; Patent No. 6107324  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic  
 ; APPLICANT: Chalmers, Derick  
 ; TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated  
 ; TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arena Pharmaceuticals, Inc.  
 ; STREET: 6166 Nancy Ridge Drive  
 ; CITY: San Diego  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92121

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/292,071  
 ; FILING DATE: April 14, 1999  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mark J. Rosen  
 ; REGISTRATION NUMBER: 39,822  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 564-6525  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 30 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 US-09-292-071-6

Query Match 67.8%; Score 12.2; DB 3; Length 30;  
 Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17  
 DB 25 TTTCACCTATCTGGAAT 9

RESULT 24  
 US-09-292-071-11/c  
 ; Sequence 11, Application US/09292071  
 ; Patent No. 6107324  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic  
 ; APPLICANT: Chalmers, Derick  
 ; TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated  
 ; TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arena Pharmaceuticals, Inc.  
 ; STREET: 6166 Nancy Ridge Drive  
 ; CITY: San Diego  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/292,071  
 ; FILING DATE: April 14, 1999  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mark J. Rosen  
 ; REGISTRATION NUMBER: 39,822  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 564-6525  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 30 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 US-09-292-071-11

Query Match 67.8%; Score 12.2; DB 3; Length 30;  
 Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17  
 | | | | | | | | | |  
 Db 25 TTTCACCTATCTGGAAT 9

RESULT 25  
 US-09-292-069A-6/c  
 ; Sequence 6, Application US/09292069A  
 ; Patent No. 6140509  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic P  
 ; APPLICANT: Chalmers, Derek T  
 ; APPLICANT: Foster, Richard J  
 ; APPLICANT: Glen, Robert C  
 ; APPLICANT: Lawless, Michael S  
 ; APPLICANT: Liaw, Chen W  
 ; APPLICANT: Liu, Qian  
 ; APPLICANT: Russo, Joseph F  
 ; APPLICANT: Smith, Julian R  
 ; APPLICANT: Thomsen, William J  
 ; TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human  
 ; TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators  
 ; TITLE OF INVENTION: Thereof  
 ; FILE REFERENCE: AREN0033  
 ; CURRENT APPLICATION NUMBER: US/09/292.069A  
 ; CURRENT FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: 60/090,783  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/112,909  
 ; PRIOR FILING DATE: 1998-12-18  
 ; PRIOR APPLICATION NUMBER: 60/123,000  
 ; PRIOR FILING DATE: 1999-03-05  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: No. 6140509el  
 ; OTHER INFORMATION: Sequence  
 ; US-09-292-069A-6

Query Match 67.8%; Score 12.2; DB 3; Length 30;  
 Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17  
 | | | | | | | | | |  
 Db 25 TTTCACCTATCTGGAAT 9

Search completed: March 3, 2006, 07:34:55  
 Job time : 24.6441 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds  
 (without alignments)  
 673.188 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18

Sequence: 1 tgtcacttatctggattt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA\_Main: \*  
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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
	1	18	100.0	18	9	US-10-182-049-22	Sequence 22, Appl
C	2	15.4	85.6	25	10	US-11-036-317-457256	Sequence 457256,
	3	14.8	82.2	25	8	US-10-719-900-965964	Sequence 965964,
C	4	14.4	80.0	25	8	US-10-719-900-661094	Sequence 661094,
	5	14	77.8	25	8	US-10-719-900-41145	Sequence 41145, A
	6	14	77.8	25	10	US-11-036-317-127763	Sequence 127763,
	7	14	77.8	25	10	US-11-036-317-746021	Sequence 746021,
	8	13.8	76.7	25	7	US-10-719-956-489627	Sequence 489627,
	9	13.8	76.7	25	7	US-10-719-956-489628	Sequence 489628,
	10	13.8	76.7	25	7	US-10-719-956-493504	Sequence 493504,
C	11	13.8	76.7	25	8	US-10-719-900-138687	Sequence 138687,
	12	13.8	76.7	25	8	US-10-719-900-398525	Sequence 398525,
C	13	13.8	76.7	25	8	US-10-719-900-426089	Sequence 426089,
C	14	13.8	76.7	25	8	US-10-719-900-443222	Sequence 443222,
	15	13.8	76.7	25	8	US-10-719-900-443223	Sequence 443223,
	16	13.8	76.7	25	8	US-10-719-900-723091	Sequence 723091,
	17	13.8	76.7	25	8	US-10-719-900-790694	Sequence 790694,
	18	13.8	76.7	25	8	US-10-719-900-901150	Sequence 901150,
	19	13.8	76.7	25	10	US-11-036-317-21790	Sequence 21790, A
	20	13.8	76.7	30	7	US-10-622-220-15	Sequence 15, Appl
	21	13.4	74.4	25	7	US-10-717-597-712	Sequence 712, App
	22	13.4	74.4	25	7	US-10-717-597-713	Sequence 713, App
	23	13.4	74.4	25	7	US-10-719-956-132748	Sequence 132748,

25	8	US-10-719-900-69367	Sequence 69367, A
25	8	US-10-719-900-359264	Sequence 359264,
25	8	US-10-719-900-383984	Sequence 383984,
25	8	US-10-719-900-557493	Sequence 557493,
25	8	US-10-719-900-870061	Sequence 870061,
25	8	US-10-719-900-966596	Sequence 966596,
25	9	US-10-809-189-102305	Sequence 102305,
25	10	US-11-036-317-462752	Sequence 462752,
25	6	US-10-291-851-8	Sequence 8, Appl1
41	3	US-09-908-975-12073	Sequence 12073, A
21	6	US-10-108-260A-4958	Sequence 4958, Ap
25	7	US-10-719-956-281385	Sequence 281385,
25	7	US-10-719-956-395340	Sequence 395340,
25	7	US-10-719-956-415591	Sequence 415591,
25	7	US-10-719-956-535367	Sequence 535367,
25	7	US-10-719-956-581172	Sequence 581172,
25	7	US-10-719-956-668305	Sequence 668305,
25	8	US-10-719-900-281343	Sequence 281343,
25	8	US-10-719-900-413325	Sequence 413325,
25	8	US-10-719-900-543959	Sequence 543959,
25	8	US-10-719-900-562112	Sequence 562112,
25	8	US-10-719-900-835724	Sequence 835724,
25	8	US-10-719-900-909419	Sequence 909419,
25	8	US-10-719-900-933964	Sequence 933964,
25	8	US-10-719-900-960944	Sequence 960944,
25	8	US-10-809-189-965963	Sequence 965963,
25	9	US-10-809-189-61721	Sequence 61721, A
25	9	US-10-809-189-111634	Sequence 111634,
25	10	US-11-036-317-27577	Sequence 27577, A
25	10	US-11-036-317-74886	Sequence 74886,
25	10	US-11-036-317-205667	Sequence 205667,
25	10	US-11-036-317-213977	Sequence 213977,
25	10	US-11-036-317-232234	Sequence 232234,
25	10	US-11-036-317-349126	Sequence 349126,
25	10	US-11-036-317-387997	Sequence 387997,
25	10	US-11-036-317-469248	Sequence 469248,
25	10	US-11-036-317-862786	Sequence 862786,
25	10	US-11-036-317-879623	Sequence 879623,
25	10	US-11-036-317-884780	Sequence 884780,
25	10	US-11-036-317-940977	Sequence 940977,
25	10	US-11-036-317-962992	Sequence 962992,
25	10	US-11-060-756-155037	Sequence 155037,
25	10	US-11-060-756-292291	Sequence 292291,
48	3	US-09-796-088-2	Sequence 2, Appl1
65	3	US-09-908-975-25634	Sequence 25634, A
25	7	US-10-719-956-182012	Sequence 182012,
25	7	US-10-719-956-495658	Sequence 495658,
25	8	US-10-719-900-237378	Sequence 237378,
25	8	US-10-719-900-392875	Sequence 392875,
25	8	US-10-719-900-800945	Sequence 800945,
25	10	US-11-036-317-469059	Sequence 469059,
25	10	US-11-036-317-559012	Sequence 559012,
25	7	US-10-681-773-71482	Sequence 71482, A
25	7	US-10-719-956-33982	Sequence 33982, A
25	7	US-10-719-956-155360	Sequence 155360,
25	7	US-10-719-956-270449	Sequence 270449,
25	7	US-10-719-956-491268	Sequence 491268,
25	7	US-10-719-956-636632	Sequence 636632,
25	8	US-10-719-900-64101	Sequence 64101, A
25	8	US-10-719-900-79886	Sequence 79886, A
25	8	US-10-719-900-179842	Sequence 179842,
25	8	US-10-719-900-438745	Sequence 438745,
25	8	US-10-719-900-482304	Sequence 482304,
25	8	US-10-719-900-661095	Sequence 661095,
25	8	US-10-719-900-901060	Sequence 901060,
25	8	US-10-719-900-920917	Sequence 920917,
25	9	US-10-956-157-237735	Sequence 237735,
25	9	US-10-843-527-46162	Sequence 46162, A
25	9	US-10-843-527-47134	Sequence 47134, A
25	9	US-10-843-527-47139	Sequence 47139, A
25	9	US-10-843-527-118490	Sequence 118490,
25	9	US-10-843-527-118758	Sequence 118758,

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c 97 12.8 71.1 25 9 US-10-843-527-118953 Sequence 118953,
98 12.8 71.1 25 9 US-10-843-527-119224 Sequence 119224,
c 99 12.8 71.1 25 9 US-10-843-527-119419 Sequence 119419,
100 12.8 71.1 25 9 US-10-843-527-119687 Sequence 119687,

ALIGNMENTS

RESULT 1
US-10-182-049-22
; Sequence 22, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-182-049-22

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGATT 18
Db 1 TGTCACCTTATCTGGATT 18

RESULT 2
US-11-036-317-457256/c
; Sequence 457256, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 457256
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-457256

Query Match 85.6%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18
Db 19 GTGCTTATCTGGATT 3

RESULT 3
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US-10-719-900-965964
; Sequence 965964, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 965964
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-965964

Query Match 82.2%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGATT 18
Db 6 TGTCACCTTATCTGGATT 23

RESULT 4
US-10-719-900-661094/c
; Sequence 661094, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 661094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-661094

Query Match 80.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
Db 18 TGACCTTATCTGGATT 3

RESULT 5
US-10-719-900-41145
; Sequence 41145, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41145
; LENGTH: 25
```



```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-41145

Query Match      77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGAT 16
Db 11 TCACCTTATCTGGAT 24

RESULT 6
US-11-036-317-127763
; Sequence 127763, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 127763
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-127763

Query Match      77.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGA 15
Db 5 GTCACCTTATCTGGA 18

RESULT 7
US-11-036-317-746021
; Sequence 746021, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 746021
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-746021

Query Match      77.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGA 15
Db 5 GTCACCTTATCTGGA 18
```

```
RESULT 8
US-10-719-956-489627
; Sequence 489627, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 489627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-489627

Query Match      76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATTT 18
Db 1 GTCACCTAATCTGATTT 17

RESULT 9
US-10-719-956-489628
; Sequence 489628, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 489628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-489628

Query Match      76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATTT 18
Db 1 GTCACCTAATCTGATTT 17

RESULT 10
US-10-719-956-493504
; Sequence 493504, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 493504
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```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-493504

Query Match      76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATTT 18
    |||||
Db 1 GTCCCGTATCTGGATTT 17
    |||||

RESULT 11
US-10-719-900-138687/c
; Sequence 138687, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 138687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-138687

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATTT 18
    |||||
Db 19 GTCTGTTATCTGGATTT 3
    |||||

RESULT 12
US-10-719-900-398525
; Sequence 398525, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 398525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-398525

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17
    |||||
Db 3 TGTCACTGATCTGGAAT 19
    |||||

RESULT 13
US-10-719-900-426089/c
; Sequence 426089, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 426089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-426089

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17
    |||||
Db 18 TATCACTTATCTGGCTT 2
    |||||

RESULT 14
US-10-719-900-443222/c
; Sequence 443222, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443222
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443222

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATTT 18
    |||||
Db 20 GTCACCTTGTCTGGTTT 4
    |||||

RESULT 15
US-10-719-900-443223/c
; Sequence 443223, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443223
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443223

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCACCTTATCTGGATT 18
      ||||| ||||| |||||
Db      20 GTCACCTTCTCTGGTTT 4

RESULT 16
US-10-719-900-723091
; Sequence 723091, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 723091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-723091

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCACCTTATCTGGATT 18
      ||||| ||||| |||||
Db      1 GTTACCTATCTGGATT 17

RESULT 17
US-10-719-900-790694
; Sequence 790694, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 790694
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-790694

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGTCACTTATCTGGATT 17
      ||||| ||||| |||||
Db      9 TGTCACTTAACTGGATT 25

RESULT 18
US-10-719-900-901150
; Sequence 901150, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 901150
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-901150

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGTCACTTATCTGGATT 17
      ||||| ||||| |||||
Db      1 TGTCACTTATCTGGATT 17

RESULT 19
US-11-036-317-21790
; Sequence 21790, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21790
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-21790

Query Match      76.7%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGTCACTTATCTGGATT 17
      ||||| ||||| |||||
Db      5 TGTGACTTCTCTGGATT 21

RESULT 20
US-10-622-220-15
; Sequence 15, Application US/10622220
; Publication No. US20040151727A1
; GENERAL INFORMATION:
; APPLICANT: Nilles, Matthew L.
; APPLICANT: Matson, Jyl S.
; TITLE OF INVENTION: YERSINIA SPECIES COMPOSITIONS
; FILE REFERENCE: 3128-60460S
; CURRENT APPLICATION NUMBER: US/10/622,220
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/444,076
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
```

```
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer, HT-YscF Start
US-10-622-220-15

Query Match      76.7%; Score 13.8; DB 7; Length 30;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 18
   |||||
Db 14 GTAACCTCTCTGGATT 30

RESULT 21
US-10-717-597-712
; Sequence 712, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 712
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-712

Query Match      74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 4 CACTTATCTGGATT 18
   |||||
Db 11 CACTGATCTGGATT 25

RESULT 22
US-10-717-597-713
; Sequence 713, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21

; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-956-132748
; Sequence 132748, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132748
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-132748

Query Match      74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 GTCACCTTATCTGGAT 16
   |||||
Db 8 GTCACCTGTCTGGAT 22

RESULT 23
US-10-719-956-132748
; Sequence 132748, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132748
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-132748

Query Match      74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 GTCACCTTATCTGGAT 16
   |||||
Db 8 GTCACCTGTCTGGAT 22

RESULT 24
US-10-719-900-69367
; Sequence 69367, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 69367
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-69367

Query Match      74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 GTCACCTTATCTGGAT 16
   |||||
Db 10 GTCACCTATCTGGAT 24
```

RESULT 25

US-10-719-900-359264  
 ; Sequence 359264, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 359264  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-359264

Query Match 74.4%; Score 13.4; DB 8; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 7e+03; 1; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGA 15  
 | | | | | | | | | | | | | | |  
 Db 3 TTTCACCTTATCTGGA 17

Search completed: March 3, 2006, 08:48:51  
 Job time : 223.11 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds  
(without alignments)  
403.294 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18

Sequence: 1 tgcacttattcgtgattt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Capext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications NA\_New.\*

- 1: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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- 6: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	15	83.3	19 10	US-11-101-244-338677 Sequence 338677
C 2	15	83.3	19 10	US-11-101-244-338777 Sequence 338777
C 3	15	83.3	19 11	US-11-083-784-338677 Sequence 338677
C 4	15	83.3	19 11	US-11-083-784-338777 Sequence 338777
C 5	14.8	82.2	19 10	US-11-101-244-1064558 Sequence 1064558
C 6	14.8	82.2	19 11	US-11-083-784-1064558 Sequence 1064558
C 7	14.8	82.2	25 12	US-11-121-849-547246 Sequence 547246
C 8	14.4	80.0	18 8	US-10-310-914A-218367 Sequence 218367
C 9	14.4	80.0	25 12	US-11-121-849-244518 Sequence 244518
C 10	14.4	80.0	50 12	US-11-175-859-7311 Sequence 7311
C 11	14.4	80.0	50 12	US-11-175-859-30578 Sequence 30578
C 12	14.4	80.0	69 8	US-10-310-914A-4848 Sequence 4848
C 13	14.4	80.0	19 10	US-11-101-244-1808 Sequence 1808
C 14	14	77.8	19 10	US-11-101-244-338658 Sequence 338658
C 15	14	77.8	19 10	US-11-101-244-338758 Sequence 338758
C 16	14	77.8	19 10	US-11-101-244-1284075 Sequence 1284075
C 17	14	77.8	19 10	US-11-083-784-1808 Sequence 1808
C 18	14	77.8	19 11	US-11-083-784-338658 Sequence 338658
C 19	14	77.8	19 11	US-11-083-784-338758 Sequence 338758
C 20	14	77.8	19 11	US-11-083-784-338758 Sequence 338758

Sequence 1284075,	19	11	US-11-083-784-1284075	77.8	14	C 21
Sequence 284878,	25	12	US-11-121-849-284878	76.7	13.8	C 22
Sequence 300225,	25	12	US-11-121-849-300225	76.7	13.8	C 23
Sequence 645767,	25	12	US-11-121-849-645767	76.7	13.8	C 24
Sequence 14753, A	50	12	US-11-175-859-14753	76.7	13.8	C 25
Sequence 77157, A	50	12	US-11-175-859-77157	76.7	13.8	C 26
Sequence 314899,	19	10	US-11-101-244-314899	74.4	27	C 27
Sequence 726306,	19	10	US-11-101-244-726306	74.4	28	C 28
Sequence 894551,	19	10	US-11-101-244-894551	74.4	29	C 29
Sequence 1304787,	19	10	US-11-101-244-1304787	74.4	30	C 30
Sequence 1587155,	19	10	US-11-101-244-1587155	74.4	31	C 31
Sequence 1587155,	19	10	US-11-101-244-1587155	74.4	32	C 32
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Sequence 726306,	19	11	US-11-083-784-726306	74.4	34	C 34
Sequence 894551,	19	11	US-11-083-784-894551	74.4	35	C 35
Sequence 1304787,	19	11	US-11-083-784-1304787	74.4	36	C 36
Sequence 1587155,	19	11	US-11-083-784-1587155	74.4	37	C 37
Sequence 123048,	25	12	US-11-121-849-123048	74.4	38	C 38
Sequence 591731,	25	12	US-11-121-849-591731	74.4	39	C 39
Sequence 41701, A	50	12	US-11-175-859-41701	74.4	40	C 40
Sequence 43502, A	50	12	US-11-175-859-43502	74.4	41	C 41
Sequence 86772, A	50	12	US-11-175-859-86772	74.4	42	C 42
Sequence 111852,	50	12	US-11-175-859-111852	74.4	43	C 43
Sequence 786862,	19	8	US-10-310-914A-786862	73.3	44	C 44
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Sequence 1385488,	19	10	US-11-101-244-1385488	73.3	46	C 46
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Sequence 984742,	21	8	US-10-310-914A-984742	73.3	49	C 49
Sequence 508577,	22	8	US-10-310-914A-508577	73.3	50	C 50
Sequence 523134,	22	8	US-10-310-914A-523134	73.3	51	C 51
Sequence 508523,	24	8	US-10-310-914A-508523	73.3	52	C 52
Sequence 508578,	25	12	US-11-121-849-508578	73.3	53	C 53
Sequence 561020,	25	12	US-11-121-849-561020	73.3	54	C 54
Sequence 603782,	25	12	US-11-175-859-603782	73.3	55	C 55
Sequence 43559, A	19	10	US-11-101-244-338688	72.2	56	C 56
Sequence 338688,	19	10	US-11-101-244-338688	72.2	57	C 57
Sequence 672128,	19	10	US-11-101-244-672128	72.2	58	C 58
Sequence 72128,	19	10	US-11-101-244-72128	72.2	59	C 59
Sequence 1449129,	19	10	US-11-101-244-1449129	72.2	60	C 60
Sequence 1449164,	19	10	US-11-101-244-1449164	72.2	61	C 61
Sequence 149165,	19	10	US-11-101-244-149165	72.2	62	C 62
Sequence 338688,	19	11	US-11-083-784-338688	72.2	63	C 63
Sequence 338788,	19	11	US-11-083-784-338788	72.2	64	C 64
Sequence 672128,	19	11	US-11-083-784-672128	72.2	65	C 65
Sequence 672225,	19	11	US-11-083-784-672225	72.2	66	C 66
Sequence 1449129,	19	11	US-11-083-784-1449129	72.2	67	C 67
Sequence 1449164,	19	11	US-11-083-784-1449164	72.2	68	C 68
Sequence 149165,	19	11	US-11-083-784-149165	72.2	69	C 69
Sequence 168002,	25	12	US-11-136-527-168002	72.2	70	C 70
Sequence 168003,	25	12	US-11-136-527-168003	72.2	71	C 71
Sequence 168008,	25	12	US-11-136-527-168008	72.2	72	C 72
Sequence 168010,	25	12	US-11-136-527-168010	72.2	73	C 73
Sequence 168021,	25	12	US-11-136-527-168021	72.2	74	C 74
Sequence 168031,	25	12	US-11-136-527-168031	72.2	75	C 75
Sequence 168031,	25	12	US-11-136-527-168031	72.2	76	C 76
Sequence 246131,	25	12	US-11-136-527-246131	72.2	77	C 77
Sequence 246131,	25	12	US-11-136-527-246131	72.2	78	C 78
Sequence 22404, A	50	12	US-11-175-859-22404	72.2	79	C 79
Sequence 62174, A	50	12	US-11-175-859-62174	72.2	80	C 80
Sequence 97672, A	19	10	US-11-101-244-97672	71.1	81	C 81
Sequence 97690, A	19	10	US-11-101-244-97690	71.1	82	C 82
Sequence 184653,	19	10	US-11-101-244-184653	71.1	83	C 83
Sequence 184655,	19	10	US-11-101-244-184655	71.1	84	C 84
Sequence 186192,	19	10	US-11-101-244-186192	71.1	85	C 85
Sequence 186223,	19	10	US-11-101-244-186223	71.1	86	C 86
Sequence 211506,	19	10	US-11-101-244-211506	71.1	87	C 87
Sequence 287716,	19	10	US-11-101-244-287716	71.1	88	C 88
Sequence 502784,	19	10	US-11-101-244-502784	71.1	89	C 89
Sequence 948857,	19	10	US-11-101-244-948857	71.1	90	C 90
Sequence 987398,	19	10	US-11-101-244-987398	71.1	91	C 91
Sequence 1064515,	19	10	US-11-101-244-1064515	71.1	92	C 92
Sequence 1218412,	19	10	US-11-101-244-1218412	71.1	93	C 93

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94 12.8 71.1 19 10 US-11-101-244-1218433 Sequence 1218433,
c 95 12.8 71.1 19 11 US-11-083-784-97672 Sequence 97672, A
c 96 12.8 71.1 19 11 US-11-083-784-97690 Sequence 97690, A
97 12.8 71.1 19 11 US-11-083-784-184653 Sequence 184653,
98 12.8 71.1 19 11 US-11-083-784-184665 Sequence 184665,
c 99 12.8 71.1 19 11 US-11-083-784-186192 Sequence 186192,
c 100 12.8 71.1 19 11 US-11-083-784-186223 Sequence 186223,

ALIGNMENTS

RESULT 1
US-11-101-244-338677/c
; Sequence 338677, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338677
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-338677

Query Match 83.3%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
Db 19 CACTTATCTGGATT 5

RESULT 2
US-11-101-244-338777/c
; Sequence 338777, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338777
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-338777

Query Match 83.3%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
Db 19 CACTTATCTGGATT 5

RESULT 3
US-11-083-784-338677/c
; Sequence 338677, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338677
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-338677

Query Match 83.3%; Score 15; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
Db 19 CACTTATCTGGATT 5

RESULT 4
US-11-083-784-338777/c
; Sequence 338777, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338777
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-338777

Query Match 83.3%; Score 15; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
Db 19 CACTTATCTGGATT 5
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RESULT 9
US-11-121-849-244518/c
; Sequence 244518, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 244518
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-244518

Query Match      80.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTCACTTATCTGGATT 17
Db      16 GTCAATTATCTGGATT 1

RESULT 10
US-11-175-859-7311/c
; Sequence 7311, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7311
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-7311

Query Match      80.0%; Score 14.4; DB 12; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGTCACCTTATCTGGATT 18
Db      36 TGTCATTATTTGGATT 19

RESULT 11
US-11-175-859-30578
; Sequence 30578, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
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; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30578
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-30578

Query Match      80.0%; Score 14.4; DB 12; Length 50;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCACCTTATCTGGATT 18
Db      3 TCAATTATCTGGATT 18

RESULT 12
US-11-175-859-30594/c
; Sequence 30594, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30594
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-30594

Query Match      80.0%; Score 14.4; DB 12; Length 50;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCACCTTATCTGGATT 18
Db      17 TCAATTATCTGGATT 2

RESULT 13
US-10-310-914A-4848
; Sequence 4848, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4848
; LENGTH: 69
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-4848

Query Match      80.0%; Score 14.4; DB 8; Length 69;
Best Local Similarity 43.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCACCTTATCTGGATT 18
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RESULT 18  
US-11-083-784-1808/c  
; Sequence 1808, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1808  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1808

Query Match 77.8%; Score 14; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14  
DB 14 TGTCACTTATCTGG 1

RESULT 19  
US-11-083-784-338658/c  
; Sequence 338658, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 338658  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-338658

Query Match 77.8%; Score 14; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14  
DB 14 TGTCACTTATCTGG 1

RESULT 20  
US-11-083-784-338758/c  
; Sequence 338758, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 338758  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-338758

Query Match 77.8%; Score 14; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14  
DB 14 TGTCACTTATCTGG 1

RESULT 21  
US-11-083-784-1284075/c  
; Sequence 1284075, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1284075  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1284075

Query Match 77.8%; Score 14; DB 11; Length 19;

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Best Local Similarity 100.0%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 TGTCACCTTATCTCG 14
    |||||
Db 14 TGTCACCTTATCTCG 1

RESULT 22
US-11-121-849-284878
; Sequence 284878, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 284878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-284878

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 2 GTCACCTTATCTCGATT 18
    |||||
Db 8 GTCACCTTATCTCGATT 24

RESULT 23
US-11-121-849-300225/c
; Sequence 300225, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 300225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-300225

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 1 TGTCACCTTATCTCGATT 17
    |||||
Db 17 TGTCACCTTATCTCGATT 1

RESULT 24
US-11-121-849-645767/c
; Sequence 645767, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 645767
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-645767

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 2 GTCACCTTATCTCGATT 18
    |||||
Db 20 GTCACCTTATCTCGATT 4

RESULT 25
US-11-175-859-14753/c
; Sequence 14753, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14753
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-14753

Query Match 76.7%; Score 13.8; DB 12; Length 50;
Best Local Similarity 88.2%; Pred. No. 7.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 2 GTCACCTTATCTCGATT 18
    |||||
Db 18 GTTACTTCTCTGGATT 2

Search completed: March 3, 2006, 07:56:44
Job time : 99.0559 secs
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***This Page Blank (uspto)***

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds  
(without alignments)  
855.220 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18  
Sequence: 1 tgcacttcttcggattt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hic: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_gsa1: \*  
10: gb\_gsa2: \*  
11: gb\_gsa3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	74.4	69	10	AG193818 Pan trogl
2	13.4	74.4	80	9	CC593206 CH240 394
3	13.2	73.3	34	10	CZ194924 PST14206-
4	13.2	73.3	52	1	AW694082 NF072C05S
5	13.2	73.3	53	10	AG201984 Pan trogl
6	13.2	73.3	62	9	BH810871 SALK 0513
7	13.2	73.3	65	3	BM886513 sam17f01
8	13.2	73.3	74	8	DN430770 LIB4217-0
9	12.8	71.1	37	8	DR1033143 JHU025B06
10	12.8	71.1	38	10	BX659120 Arabidops
11	12.8	71.1	57	7	CV519718 0089P0033
12	12.8	71.1	57	11	CR249388 Reverse s
13	12.8	71.1	68	11	CR111866 Forward s
14	12.8	71.1	77	9	AZ374283 CR249388
15	12.8	71.1	77	9	BH643554 1008058F0
16	12.8	71.1	78	1	AL796390 AL796390
17	12.4	68.9	24	9	AZ303688 1M0003M11
18	12.4	68.9	62	3	BP080139 BP080139
19	12.4	68.9	74	1	AV963593 AV963593
20	12.2	67.8	42	11	TA92F10Q AL462451 T. brucei
21	12.2	67.8	50	1	AI308308 ta90f01.x
22	12.2	67.8	54	9	AQ073921 BP(3)3330

23	12.2	67.8	56	9	AZ469856 1M0283B08
24	12.2	67.8	59	11	CR061632 Reverse s
25	12.2	67.8	60	6	CD940007 RAA 94 Ge
26	12.2	67.8	60	6	CD948191 SAD 45 Ge
27	12.2	67.8	60	6	CD948787 SAH 116 G
28	12.2	67.8	61	6	CB298000 12B22006
29	12.2	67.8	62	7	CN545516 EST 17460
30	12.2	67.8	64	9	BZ353869 SALK 1222
31	12.2	67.8	67	10	CW990741 BB0131 Sa
32	12.2	67.8	68	9	AZ348360 1M0084E11
33	12.2	67.8	73	6	CD928058 GR45 1030
34	12.2	67.8	74	6	CD957750 SCL 33 Ge
35	12.2	67.8	74	11	DQ044542 Pan trogl
36	12.2	67.8	76	9	AZ824720 2M0099D01
37	12.2	67.8	77	11	DQ044541 Homo sapi
38	12.2	67.8	79	10	AL944230 Arabidops
39	12	66.7	63	10	CG507308 OST57211
40	12	66.7	73	7	CF845484 p8HB033XC
41	11.8	65.6	37	1	AA500031 v196e11.1
42	11.8	65.6	42	10	CZ487542 f04956-3p
43	11.8	65.6	46	9	BZ663309 SALK 0269
44	11.8	65.6	48	9	BH847074 SALK 0130
45	11.8	65.6	51	9	AZ604141 1M0423B23
46	11.8	65.6	56	1	AJ929315 AJ929315
47	11.8	65.6	56	1	AJ935185 AJ935185
48	11.8	65.6	59	1	AJ935523 AJ935523
49	11.8	65.6	62	6	CF292190 14ROOT--0
50	11.8	65.6	62	9	CF793802 SALK 0186
51	11.8	65.6	62	9	CF793802 SALK 0186
52	11.8	65.6	64	9	BH220392 1006094C0
53	11.8	65.6	66	6	CD391037 Gm CK0466
54	11.8	65.6	66	9	AZ360386 1M0103C11
55	11.8	65.6	67	1	AA878568 o117b07.8
56	11.8	65.6	68	9	AZ962147 2M0230C21
57	11.8	65.6	68	9	BH810780 SALK 0511
58	11.8	65.6	68	9	BH846857 SALK 0107
59	11.8	65.6	69	9	AZ615106 1M0444H14
60	11.8	65.6	75	10	AL946811 Arabidops
61	11.8	65.6	76	1	AI609425 tt82a07.x
62	11.8	65.6	76	2	BE857854 7d60c08.x
63	11.8	65.6	76	8	DN336290 LIB3187-0
64	11.8	65.6	76	9	BH855752 SALK 0847
65	11.8	65.6	77	10	BX292494 Arabidops
66	11.8	65.6	77	11	CR034215 Forward s
67	11.8	65.6	79	1	AA623234 v114f04.1
68	11.8	65.6	79	8	Z21465 HSAABE1NM T
69	11.8	65.6	79	10	AL940313 Arabidops
70	11.6	64.4	26	10	CG722225 1119071A0
71	11.6	64.4	35	9	AZ428773 1M0212123
72	11.6	64.4	35	9	BH908235 SALK 0466
73	11.6	64.4	36	10	AJ593904 Arabidops
74	11.6	64.4	37	1	AU258765 AU258765
75	11.6	64.4	39	9	BZ381294 SALK 1165
76	11.6	64.4	43	9	BH790170 SALK 0546
77	11.6	64.4	44	7	CV293350 EST881727
78	11.6	64.4	45	9	BZ384356 SALK 1354
79	11.6	64.4	46	8	D18692 MUSGS01754
80	11.6	64.4	46	3	BM889473 laa02905
81	11.6	64.4	51	9	AZ776863 2M0010E20
82	11.6	64.4	51	9	AZ797131 2M0053K12
83	11.6	64.4	53	9	BH810529 SALK 0497
84	11.6	64.4	53	9	BH810530 SALK 0497
85	11.6	64.4	53	9	BZ662063 SALK 0255
86	11.6	64.4	54	11	DE000867 Branchios
87	11.6	64.4	55	9	BZ354029 SALK 1225
88	11.6	64.4	55	10	CL301069 03S061-0
89	11.6	64.4	56	9	CC795632 SALK 0876
90	11.6	64.4	57	11	CR250663 Forward s
91	11.6	64.4	58	8	D18271 MUSGS00467
92	11.6	64.4	58	9	AZ789582 2M0037E05
93	11.6	64.4	59	9	AZ591500 1M0401D11
94	11.6	64.4	59	10	AJ595268 Arabidops
95	11.6	64.4	60	6	CB217727 NISC_nb04

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96      11.6   64.4   61   1   AA845045   AA845045 ak58b04.s
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c 98      11.6   64.4   64   8   DN878559   DN878559 nae2id02
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                                ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-071D13.T7, genomic survey
sequence.
ACCESSION AG193818
VERSION AG193818.1 GI:45225994
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE 1
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 69)
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
TITLE Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daegu 305-333, Korea
(E-mail:redstone@mail.krribb.re.kr, URL:http://phs.grc.krribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="RP43-071D13.T7"
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/cell_type="lymphocytes"
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ORIGIN
Query Match 74.4%; Score 13.4; DB 10; Length 69;
Best Local Similarity 93.3%; Pred. No. 4.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
|||||
Db 8 CACTTATATGGATT 22

RESULT 2
CC593206
LOCUS
DEFINITION CH240_394G6.TABAC13P2 CHORI-240 Bos taurus genomic clone
CH240_394G6, genomic survey sequence.
ACCESSION CC593206
VERSION CC593206.1 GI:31952671

                                ALIGNMENTS

RESULT 3
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LOCUS
DEFINITION PST14206-NR MICB1 Mus musculus genomic clone PST14206-NR, genomic
survey sequence.
ACCESSION CC593206
VERSION CC593206.1 GI:58833368
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 34)
Hicks,G.G.

```

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GSS.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 80)
Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Chiu,R.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: CH240_394G6.T7
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 394 row: G column: 6
Seq primer: SP6
Class: BAC ends.
FEATURES
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/sex="Male"
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/notes="Vector: pTABAC1.3; Site 1: MboI; Site 2: MboI;
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Library (Male) produced by Pieter de Jong"
ORIGIN
Query Match 74.4%; Score 13.4; DB 9; Length 80;
Best Local Similarity 93.3%; Pred. No. 5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
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Db 64 CACATATCTGGATT 78

RESULT 3
CC593206
LOCUS
DEFINITION PST14206-NR MICB1 Mus musculus genomic clone PST14206-NR, genomic
survey sequence.
ACCESSION CC593206
VERSION CC593206.1 GI:58833368
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 34)
Hicks,G.G.

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TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1985, Vol. 10, No. 2, pp. 1-15
3. The Importance of Parental Involvement	Journal of Educational Psychology	1990, Vol. 82, No. 3, pp. 1-12
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1995, Vol. 98, No. 4, pp. 1-18
5. The Role of the School in the Community	Journal of Educational Research	2000, Vol. 103, No. 5, pp. 1-20
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2005, Vol. 108, No. 6, pp. 1-25
7. The Role of the Teacher in the 21st Century	Journal of Educational Research	2010, Vol. 113, No. 7, pp. 1-30
8. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2015, Vol. 118, No. 8, pp. 1-35
9. The Role of the Teacher in the 21st Century	Journal of Educational Research	2020, Vol. 123, No. 9, pp. 1-40
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2025, Vol. 128, No. 10, pp. 1-45

www.EScells.ca  
Unpublished (2002)  
Contact: Hicks GG  
Mammalian Functional Genomics Centre  
Manitoba Institute of Cell Biology, University of Manitoba  
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada  
Tel: 204 787 2133  
Fax: 204 787 2190  
Email: hicksgg@cc.umanitoba.ca  
US3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional  
sequence information and target gene cloning can be generated. ES  
cell line harboring insertion mutation of target gene is available.  
Sequence analysis available from  
'http://340.193.242.7/esdb/PSTreport.php?PST=PST14206-NR'  
Clasp: Gene Trap.

**FEATURES**  
**SOURCE**

## ORIGIN

Query Match 73.3%; Score 13.2; DB 10; Length 34;  
Best Local Similarity 83.3%; Pred. No. 5.8e+04;  
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/clone_lib="Developing
/note="Vector: Lambda
internodal stem segme

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## ORIGIN

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Best Local Similarity 83.3%;
Pred. No. 6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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## ORIGIN

Query Match 73.3%; Score 13.2; DB 10; Length 53;  
Best Local Similarity 83.3%; Pred. No. 6.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0 Gaps 0;

**FEATURES**  
**SOURCE**

**RESULT 6**  
**BM810871/c**  
**LOCUS**  
**DEFINITION** SALK\_051322 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_051322, genomic survey sequence.  
**ACCESSION** BM810871  
**VERSION** BM810871.1 GI:20388689  
**KEYWORDS** GSS.  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
**REFERENCE** 1 (bases 1 to 62)  
**AUTHORS** Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.  
**TITLE** A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At2g33540.  
**CLASS:** TDNA tagged.  
**FEATURES**  
 source  
 1..62  
 /location="Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_051322"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
**ORIGIN**  
 Query Match 73.3%; Score 13.2; DB 9; Length 62;  
 Best Local Similarity 83.3%; Pred.No. 6.2e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TGTCACCTTATCTGGATT 18  
 ||| ||||| ||||| |||||  
 Db 52 TGTAAATATCTGGTTT 35  
**RESULT 7**  
**BM886513**  
**LOCUS**  
**DEFINITION** sam17f01.y1 Gm-c1068 Glycine max cDNA clone SOYBEAN CLONE ID:  
**ACCESSION** Gm-c1068-5233 5', mRNA sequence.  
**VERSION** BM886513  
**KEYWORDS** BM886513.1 GI:19270257  
**SOURCE** EST.  
 Glycine max (soybean)  
**ORGANISM** Glycine max  
**REFERENCE** 1 (bases 1 to 65)  
**AUTHORS** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
**TITLE** 1 (bases 1 to 65)  
**AUTHORS** Direct Submission (Staten,N.R.)  
**TITLE** Direct Submission (Staten,N.R.)

**AUTHORS** Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, F., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
**TITLE** Public Soybean EST Project  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: [info@biogeneticservices.com](mailto:info@biogeneticservices.com))  
 Putative full length read vector to vector length is 66  
 Seq primer: -40RP from Gibco.  
**FEATURES**  
 Location/Qualifiers  
 1..65  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /culturvar="Williams 82"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-c1068-5233"  
 /issue\_type="Leaf, drought stressed, 1 month old plants, greenhouse grown"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-c1068"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

**ORIGIN**  
 Query Match 73.3%; Score 13.2; DB 3; Length 65;  
 Best Local Similarity 83.3%; Pred.No. 6.2e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TGTCACCTTATCTGGATT 18  
 ||| ||||| ||||| |||||  
 Db 23 TGTCACCTTATCTGTATAT 40  
**RESULT 8**  
**DN430770**  
**LOCUS**  
**DEFINITION** DN430770 74 bp mRNA linear EST 08-MAR-2005  
**ACCESSION** LIB4217-011-R1-K1-G5 LIB4217 Canis familiaris cDNA clone  
**VERSION** CLN10755221, mRNA sequence.  
**KEYWORDS** DN430770  
**SOURCE** DN430770.1 GI:60627015  
 EST.  
 Canis familiaris (dog)  
**ORGANISM** Canis familiaris  
**REFERENCE** 1 (bases 1 to 74)  
**AUTHORS** Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.  
**TITLE** 1 (bases 1 to 74)  
**AUTHORS** Direct Submission (Staten,N.R.)  
**TITLE** Direct Submission (Staten,N.R.)

JOURNAL Unpublished (2005)  
 COMMENT Contact: Nick Staten  
 Tel: 636 247 6855  
 Email: nicholas.r.staten@fizer.com.

FEATURES  
 source Location/Qualifiers  
 1..74  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /strain="beagle"  
 /db\_xref="taxon:9615"  
 /clone="CLN10755221"  
 /tissue\_type="left atrium"  
 /lab\_host="DH108"  
 /clone\_lib="LIB4217"  
 /notes="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; mixed"

ORIGIN  
 Query Match 73.3%; Score 13.2; DB 8; Length 74;  
 Best Local Similarity 83.3%; Pred. NO. 6.3e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18  
 |||||  
 Db 38 TTTTACTTATCTGGATT 55

RESULT 9  
 DR103143  
 LOCUS 37 bp mRNA linear EST 13-JUN-2005  
 DEFINITION JHU025B06L37 Canine cardiovascular system biased cDNA Canis familiaris cDNA, mRNA sequence.

ACCESSION DR103143  
 VERSION DR103143.1 GI:67562498  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 37)  
 AUTHORS DiSilvestre D., Yung C., Gao Z., Farukhi Y., Winslow R.L. and Tomaselli G.F.  
 TITLE Canine cardiovascular system biased cDNA sequences  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Gordon F. Tomaselli  
 Johns Hopkins University  
 720 Rutland Avenue/Ross 844, Baltimore, MD 21205, USA  
 Tel: 4109552774  
 Fax: 4105022096  
 Email: gtomasel@jhmi.edu.

FEATURES  
 source Location/Qualifiers  
 1..37  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /strain="Mixed"  
 /db\_xref="taxon:9615"  
 /sex="Mixed"  
 /clone\_lib="Canine cardiovascular system biased cDNA"  
 /note="Organ: Mixed; Vector: pCDNA3.1; Site\_1: EcoRI; Site\_2: XhoI; Adult tissue from eye, lung, aorta, pulmonary artery and brain; neonatal tissue from liver, spleen, thymus, lung, kidney, aorta and brain; 50% is from cardiac tissues."

ORIGIN  
 Query Match 71.1%; Score 12.8; DB 8; Length 37;  
 Best Local Similarity 87.5%; Pred. NO. 9.4e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18  
 |||||  
 Db 16 TCACCTTATCTGGATT 31

RESULT 10  
 BX659120/c  
 LOCUS 38 bp DNA linear GSS 04-APR-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-643A04-022303, genomic survey sequence.

ACCESSION BX659120  
 VERSION BX659120.1 GI:37615508  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE 1  
 Li Y., Rosso M.G., Strizhov N., Viehoveer P. and Weisshaar B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 12874060

2  
 Rosso M.G., Li Y., Strizhov N., Reiss B., Dekker K. and Weisshaar B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321

3  
 Strizhov N., Li Y., Rosso M.G., Viehoveer P., Dekker K.A. and Weisshaar B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14692050

4 (bases 1 to 38)  
 Rosso M.G., Strizhov N., Li Y. and Weisshaar B.  
 Direct Submission  
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g05420. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers  
 1..38  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-643A04-022303"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

FEATURES  
 source  
 Query Match 71.1%; Score 12.8; DB 10; Length 38;  
 Best Local Similarity 87.5%; Pred. NO. 9.4e+04;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 17  
 |||||  
 Db 34 GTGACTTATCTGGATT 19

# ORIGIN

```

RESULT 11
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:53846250
KEYWORDS
EST.
SOURCE
Mimulus guttatus (spotted monkey flower)
ORGANISM
Mimulus guttatus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Lamiales; Phrymaceae; Mimulus.
1 (bases 1 to 57)
Willis, J., Vision, T., Dietrich, P.S. and Allen, A.
Mimulus guttatus cDNA sequence
Unpublished (2004)
Contact: Willis J
Department of Biology
Duke University
072-A Biological Sciences Science Drive, Durham, NC 27708, USA
Tel: 919 660 7340
Fax: 919 660 7293
Email: jwillis@duke.edu
Plate: 0089P0033 row: 01 column: D
Seq primer: T7
High quality sequence start: 15
High quality sequence stop: 622.
Location/Qualifiers
1..57
/organism="Mimulus guttatus"
/mol_type="mRNA"
/db_xref="taxon:4155"
/clone="0089P00332.x0_D01"
/clone_lib="Mimulus guttatus library 2"
/note="Vector: pGEM-T Easy; a Mimulus guttatus cDNA
library"

FEATURES
source
1..57
/db_xref="taxon:10090"
/clone="MHPN311c07"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 7; Length 57;
Best Local Similarity 87.5%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACTTATCTGGATT 17
Db 52 GTTCTTATCTGGATT 37

RESULT 12
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:50028241
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 57)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
1..57
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN311c07"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 7; Length 57;
Best Local Similarity 87.5%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACTTATCTGGATT 17
Db 52 GTTCTTATCTGGATT 37

RESULT 13
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:50028241
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 57)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
1..57
/organism="Mus musculus"
/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
Db 29 TGCCACATATCTGGAT 44

RESULT 14
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:10487983
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, W., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Location/Qualifiers
1..77
/organism="Mus musculus"
/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
Db 29 TGCCACATATCTGGAT 44

RESULT 15
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:10487983
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, W., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Location/Qualifiers
1..77
/organism="Mus musculus"
/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
Db 29 TGCCACATATCTGGAT 44

```

```

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 57;
Best Local Similarity 87.5%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACTTATCTGGATT 18
Db 9 TCACTAATCTGGACTT 24

RESULT 13
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:49859281
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 68)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
1..68
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN311c07"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
Db 29 TGCCACATATCTGGAT 44

RESULT 14
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:10487983
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, W., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Location/Qualifiers
1..77
/organism="Mus musculus"
/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
Db 29 TGCCACATATCTGGAT 44

RESULT 15
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0089P00332.x0_D01, mRNA sequence.
CV519718
ACCESSION
CV519718.1 GI:10487983
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, W., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Location/Qualifiers
1..77
/organism="Mus musculus"
/mol_type="genomic DNA"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
Db 29 TGCCACATATCTGGAT 44

```

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0126 row: 1 column: 19  
Seq primer: CACACGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 77.

## FEATURES

source

1. .77  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIW0126119"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIW library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 71.1%; Score 12.8; DB 9; Length 77;  
Best Local Similarity 87.5%; Pred. No. 1e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACTTATCTGGATT 18

|||||  
57 TCACATATCTGGCTTT 72

Db

## RESULT 15

BH643554/c

LOCUS

DEFINITION BH643554 77 bp DNA linear GSS 14-FEB-2002  
survey sequence.

ACCESSION

BH643554

VERSION

BH643554.1

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Zea mays

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 77)

Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

## FEATURES

source

1. .77  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/Al88/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1008 - RescueMu Grid I"  
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 71.1%; Score 12.8; DB 9; Length 77;  
Best Local Similarity 87.5%; Pred. No. 1e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTATCTGGATT 17

|||||  
24 GTCACCTATCTGGATT 9

Db

## RESULT 16

AL796390/c

LOCUS

DEFINITION AL796390 XGC-neurula Xenopus tropicalis cDNA clone TNeul28114 5',  
mRNA sequence.

ACCESSION

AL796390

VERSION

AL796390.2

KEYWORDS

EST.

SOURCE

Xenopus tropicalis (western clawed frog)

ORGANISM

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 78)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2001 (11\_2003)

Unpublished (2003)

On Jun 25, 2002 this sequence version replaced gi:21582094.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula.

EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the

5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli DH10B

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TNeul28114.picSP6

Sequencing primer: SP6.

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008058 row: 11

Class: transposon-tagged.

```

FEATURES
  source
    Location/Qualifiers
      1..78
        /organism="Xenopus tropicalis"
        /mol_type="mRNA"
        /db_xref="taxon:9364"
        /clone="TNeu128114"
        /dev_stage="neureula"
        /lab_host="Escherichia coli DH10B"
        /clone_lib="XGC-neureula"
        /notes="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
        was oligo dT primed from Sug of poly A+ RNA from neurula.
        EcoRI-NotI cut cDNA was then ligated into pCS107 with
        EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
  Query Match      71.1%; Score 12.8; DB 1; Length 78;
  Best Local Similarity 87.5%; Pred. No. 1e+05;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3 TCACCTTATCTGGATTT 18
    |||||
Db  44 TCACCTCTCAGGATTT 29

RESULT 17
LOCUS      AZ303688                24 bp    DNA        linear    GSS 29-SEP-2000
DEFINITION  IM0003M11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0003M11 F, genomic survey sequence.
ACCESSION  AZ303688
VERSION    AZ303688.1  GI:10339066
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Mus.
            1 (bases 1 to 24)
REFERENCE  1
  AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL  Unpublished (2000)
  COMMENT  Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0003 row: M column: 11
            Seq primer: CGTGTAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
            Location/Qualifiers
              1..24
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0003M11"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="vector: pMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a

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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
  Query Match      68.9%; Score 12.4; DB 9; Length 24;
  Best Local Similarity 92.9%; Pred. No. 1.4e+05;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  5 ACTTATCTGGATTT 18
    |||||
Db  5 ACTTATCTGGATAT 18

RESULT 18
LOCUS      BP080139                62 bp    mRNA        linear    EST 27-AUG-2004
DEFINITION  cDNA clone MR054b08_f 3', mRNA sequence.
ACCESSION  BP080139
VERSION    BP080139.1  GI:45636800
KEYWORDS   EST.
SOURCE     Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM   Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
            Lotus.
            1 (bases 1 to 62)
REFERENCE  1
  AUTHORS  Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE    Characteristics of the Lotus japonicus gene repertoire deduced from
            large-scale expressed sequence tag (EST) analysis
            Plant Mol. Biol. 54 (3), 405-414 (2004)
  JOURNAL  15284495
  COMMENT  Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
            Location/Qualifiers
              1..62
                /organism="Lotus corniculatus var. japonicus"
                /mol_type="mRNA"
                /isolate="Miyakojima MG-20"
                /db_xref="taxon:34305"
                /clone="MR054b08_f"
                /tissue_type="roots"
                /clone_lib="Lotus japonicus roots"

ORIGIN
  Query Match      68.9%; Score 12.4; DB 3; Length 62;
  Best Local Similarity 92.9%; Pred. No. 1.6e+05;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3 TCACCTTATCTGGAT 16
    |||||
Db  39 TCACCTTCTGGAT 52

RESULT 19
LOCUS      AV963593                74 bp    mRNA        linear    EST 14-MAR-2002

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DEFINITION AV963593 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone cieg24107 5', mRNA sequence.
ACCESSION AV963593
VERSION AV963593.1 GI:19451892
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1.74
Location/Qualifiers
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg24107"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 68.9%; Score 12.4; DB 1; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTTATCTGGATT 18
| | | | | | | | | |
Db 18 ATTATCTGGATT 31

RESULT 20
TA92F10Q
LOCUS TA92F10Q 42 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 92f10, reverse sequence,
genomic survey sequence.
ACCESSION AL462451
VERSION AL462451.1 GI:11862749
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
REFERENCE Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
1 (bases 1 to 42)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
JOURNAL Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..42
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="92f10"

ORIGIN
Query Match 67.8%; Score 12.2; DB 11; Length 42;
Best Local Similarity 82.4%; Pred. No. 1.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
| | | | | | | | | |
Db 5 TGCCCTTATCTGGCTT 21

RESULT 21
AI308308/c
LOCUS AI308308 50 bp mRNA linear EST 10-DEC-1998
DEFINITION ta90f01.x1 NCI CGAP Brn20 Homo sapiens cDNA clone IMAGE:2051353 3',
similar to gb:M54927 MYELIN PROTEOLIPID PROTEIN (HUMAN);, mRNA
sequence.
ACCESSION AI308308
VERSION AI308308.1 GI:4002943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 50)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(TCGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2051353"
/tissue_type="oligodendrogloma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn20"
/note="Organ: brain; Vector: pAMP1; mRNA made from
oligodendrogloma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

ORIGIN
Query Match 67.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 TGTCACTTATCTGGATT 17
    ||||| ||||| |||||
Db 37 TGTCACTTATCTGGATT 21

RESULT 22
AQ073921/c
LOCUS
DEFINITION EP(3)330 Drosophila melanogaster EP line Drosophila melanogaster
genomic sequence recovered from Both 5' and 3' ends of P element,
genomic survey sequence.
ACCESSION AQ073921
VERSION AQ073921.1 GI:3403963
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 54)
AUTHORS Liao, G.-C., Rehm, E.J. and Rubin, G.M.
TITLE Insertion site preferences of the P transposable element in
Drosophila melanogaster
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
PUBMED 10716700
COMMENT Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P
element

The P element insertion position is base 19 in the 54 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1. 54
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/notes="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains a single EP
transposable element insertion. (The generation of these
insertion strains is described in Rorth P, Szabo K, Bailey
A, Laverly T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
genetics in Drosophila. Development 6:1049-1057.) The
resultant fragment for each strain was directly sequenced
to determine the genomic sequence at the site of
insertion. Details of the protocols used can be found at
http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

ORIGIN
Query Match 67.8%; Score 12.2; DB 9; Length 54;
Best Local Similarity 82.4%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATT 18
    ||||| ||||| |||||
Db 22 GACACCTTATCTGGCTTT 6

RESULT 23
AZ469856
LOCUS
DEFINITION AZ469856 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0283B08 R, genomic survey sequence.

ACCESSION AZ469856
VERSION AZ469856.1 GI:10627981
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 56)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0283 row: B column: 08
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 56.
Location/Qualifiers
1. 56
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0283B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 67.8%; Score 12.2; DB 9; Length 56;
Best Local Similarity 82.4%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATT 18
    ||||| ||||| |||||
Db 1 GGCACCTGCTCGATT 17

RESULT 24
CR061632/c
LOCUS
DEFINITION CR061632 Reverse strand read from insert in 3'HPRT insertion targeting and

```



chromosome engineering clone MHPPI28G02, genomic survey sequence.  
 CR061632 1 GI:49795104  
 GSS: genome survey sequence; MICR.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 59)  
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>

FEATURES  
 source 1..59  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="MHPPI28G02"  
 /clone\_lib="MHPP"

## ORIGIN

Query Match 67.8%; Score 12.2; DB 11; Length 59;  
 Best Local Similarity 82.4%; Pred. No. 2e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18  
 |||||

DB 49 GTCCCTATCAGGATT 33  
 |||||

## RESULT 25

CD940007  
 LOCUS CD940007 60 bp mRNA linear EST 15-JUL-2003  
 DEFINITION RAA\_94 GenTag1 Zea mays cDNA, mRNA sequence.  
 ACCESSION CD940007  
 VERSION CD940007.1 GI:32787515  
 KEYWORDS EST.

SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 60)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
 and <http://genoplante-info.infobiogen.fr>).

## FEATURES

source 1..60  
 Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="mixture"  
 /db\_xref="taxon:4577"  
 /clone\_lib="GenTag1"

## ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 60;  
 Best Local Similarity 82.4%; Pred. No. 2e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17  
 |||||

Db 20 TGTCACTTCACTGGAAT 36

Search completed: March 3, 2006, 11:01:40  
 Job time : 989.737 secs

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